

GenCore version 4.5
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On nucleic - nucleic search, using sw model
Run on: August 26, 2002, 21:20:54 ; Search time 1915.63 Seconds
(without alignments)
229.406 Million cell updates/sec

Title: US-10-037-990A-3

Perfect score: 21

Sequence: 1 gtcgtgcagccctccaggacc 21

Scoring table: OLIGO_NUC

Gapop 60.0 , Gapext 60.0

Searched: 1797656 seqs, 10463268293 residues

Word size : 21

Total number of hits satisfying chosen parameters:

10

Minimum DB seq length: 0

Maximum DB seq length: 100

Post-processing: Listing first 65 summaries

Database : GenEmpi:*

1: qb_ba:*

2: qb_htg:*

3: qb_in:*

4: qb_on:*

5: qb_ov:*

6: qb_pat:*

7: qb_ph:*

8: qb_pl:*

9: qb_pr:*

10: qb_ro:*

11: qb_sts:*

12: qb_sy:*

13: qb_un:*

14: qb_vl:*

15: em_ba:*

16: em_fun:*

17: em_hum:*

18: em_in:*

19: em_mu:*

20: em_on:*

21: em_or:*

22: em_oxv:*

23: em_pat:*

24: em_Ph:*

25: em_Pl:*

26: em_ro:*

27: em_sts:*

28: em_un:*

29: em_vl:*

30: em_htq_hum:*

31: em_htq_inv:*

32: em_htq_other:*

33: em_htgo_inv:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
8				

RESULTS

ALIGNMENTS

RESULT	1	REF ID	AX147016	DEFINITION	Sequence 10 from Patent WO0137291.	ACCESSION	AX147016	VERSION	AX147016.1	GI	14346287	DNA	linear	PAT	08-JUN-2001	
JOURNAL				Roche Diagnostics GmbH (DE)												
FEATURES				Location/Qualifiers												
source				1..21												
				/organism="Synthetic construct"												
				/db_xref="taxon:2630"												
				/note="Synthetic oligonucleotide probe (HCV)"												
				modified_base												
BASE COUNT	3	a	9	c	9	OTHER	6	g	9	t	3					
ORIGIN																
Query Match	100.0%		Score	21	DB	6	Length	21								
Best Local Similarity	100.0%		Prod. No.	0.042												
Matches	21		Mismatches	0			Indels	0		Gaps	0					
QY	1	gtcgtgcagccctccaggacc	21													
Db	1	GTCTGTCAGCCCTCCAGGACC	21													
RESULT	2	BD000273/c														
LOCUS		BD000273														
DEFINITION		Oligonucleotide primers for efficient detection of hepatitis C virus (HCV) and methods of use thereof.														
ACCESSION		BD000273														
VERSION		BD000273.1														
KEYWORDS		JP 2000279200-A/11.														
SOURCE																
ORGANISM																
REFERENCE																
AUTHORS		Lynen,J.M. and Gorman,K.M.														
TITLE		Oligonucleotide primers for efficient detection of hepatitis C virus (HCV) and methods of use thereof														
JOURNAL																
COMMENT		Patent: JP 2000279200-A/11-05-OCT-2000;														
PN		ORTHO CLINICAL DIAGNOSTICS INC														
PD		Artificial Sequence														
PF		JP 2000279200-A/11-10-OCT-2000														
PP		03-FEB-2000														
PF		JP 2000032656														

03-08-2001

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BASE COUNT	9 a	17 c	14 g	8 t	ORIGIN
Query Match	100.0%	Score 21;	DB 6;	Length 48;	
Best Local Similarity	100.0%	Pred. No.	0.039;	Mismatches	0;
Matches	21;	Conservative	0;	Indels	0;
Qy	1 gtctgttcaggccctccaggaccc	21			
Db	10 GTCGTCAGCCTCCAGGACCC	30			
RESULT	7				
AX021575	AX021575	Sequence 13 from Patent	48 bp	DNA	linear
DEFINITION		WO9924606.			PAT 07-SEP-2000
ACCESSION	AX021575				
VERSION	AX021575.1	GI:10044859			
KEYWORDS					
SOURCE		synthetic construct.			
ORGANISM		synthetic construct.			
REFERENCE		artificial sequence.			
AUTHORS	Kessler,C., Bartl,K., Haberhausen,G. and Orum,H.				
TITLE	Specific and sensitive nucleic acid detection method				
JOURNAL	Patent: WO 9924606-A 13 20-MAY-1999;				
ROCHE DIAGNOSTICS GMBH (DE); ORUM HENRIK (DK)					
FEATURES	Location/Qualifiers				
source	1. .48 '/organism="synthetic construct" '/db_xref="taxon:32630" '/note="HCV_2B"				
BASE COUNT	9 a	18 c	14 g	7 t	ORIGIN
ORIGIN					
Query Match	100.0%	Score 21;	DB 6;	Length 48;	
Best Local Similarity	100.0%	Pred. No.	0.039;	Mismatches	0;
Matches	21;	Conservative	0;	Indels	0;
Qy	1 gtctgttcaggccctccaggaccc	21			
Db	10 GTCGTCAGCCTCCAGGACCC	30			
RESULT	8				
AX021576	AX021576	Sequence 14 from Patent	48 bp	DNA	linear
DEFINITION	WO9924606.				PAT 07-SEP-2000
ACCESSION	AX021576				
VERSION	AX021576.1	GI:10044860			
KEYWORDS					
SOURCE		synthetic construct.			
ORGANISM		synthetic construct.			
REFERENCE		artificial sequence.			
AUTHORS	Kessler,C., Bartl,K., Haberhausen,G. and Orum,H.				
TITLE	Specific and sensitive nucleic acid detection method				
JOURNAL	Patent: WO 9924606-A 14 20-MAY-1999;				
ROCHE DIAGNOSTICS GMBH (DE); ORUM HENRIK (DK)					
FEATURES	Location/Qualifiers				
source	1. .48 '/organism="synthetic construct" '/db_xref="taxon:32630" '/note="HCV_MCR":32630"				
BASE COUNT	9 a	17 c	14 g	8 t	ORIGIN
ORIGIN					
Query Match	100.0%	Score 21;	DB 6;	Length 48;	
Best Local Similarity	100.0%	Pred. No.	0.039;	Mismatches	0;
Matches	21;	Conservative	0;	Indels	0;
Qy	1 gtctgttcaggccctccaggaccc	21			
Db	10 GTCGTCAGCCTCCAGGACCC	30			
RESULT	9				
AX021631	AX021631	Sequence 10 from Patent	48 bp	DNA	linear
DEFINITION	WO9923250.				PAT 07-SEP-2000
ACCESSION	AX021631				
VERSION	AX021631.1	GI:10044914			
KEYWORDS					
SOURCE		synthetic construct.			
ORGANISM		synthetic construct.			
REFERENCE		artificial sequence.			
AUTHORS	Kessler,C., Bartl,K., Haberhausen,G. and Orum,H.				
TITLE	Specific and sensitive method for detecting nucleic acids				
JOURNAL	Patent: WO 9923250-A 10 14-MAY-1999;				
ROCHE DIAGNOSTICS GMBH (DE); BARTL KURT (DE); HABERHAUSEN GERD (DE); KESSLER CHRISTOPH (DE)					
FEATURES	Location/Qualifiers				
source	1. .48 '/organism="synthetic construct" '/db_xref="taxon:32630" '/note="HCV_2B"				
BASE COUNT	9 a	18 c	14 g	7 t	ORIGIN
ORIGIN					
Query Match	100.0%	Score 21;	DB 6;	Length 48;	
Best Local Similarity	100.0%	Pred. No.	0.039;	Mismatches	0;
Matches	21;	Conservative	0;	Indels	0;
Qy	1 gtctgttcaggccctccaggaccc	21			
Db	10 GTCGTCAGCCTCCAGGACCC	30			
RESULT	10				
AX021632	AX021632	Sequence 11 from Patent	48 bp	DNA	linear
DEFINITION	WO9923250.				PAT 07-SEP-2000
ACCESSION	AX021632				
VERSION	AX021632.1	GI:10044915			
KEYWORDS					
SOURCE		synthetic construct.			
ORGANISM		synthetic construct.			
REFERENCE		artificial sequence.			
AUTHORS	Kessler,C., Bartl,K., Haberhausen,G. and Orum,H.				
TITLE	Specific and sensitive method for detecting nucleic acids				
JOURNAL	Patent: WO 9923250-A 11 14-May-1999;				
ROCHE DIAGNOSTICS GMBH (DE); BARTL KURT (DE); HABERHAUSEN GERD (DE); KESSLER CHRISTOPH (DE)					
FEATURES	Location/Qualifiers				
source	1. .48 '/organism="synthetic construct" '/db_xref="taxon:32630" '/note="HCV_MCR":32630"				
BASE COUNT	9 a	17 c	14 g	8 t	ORIGIN
ORIGIN					
Query Match	100.0%	Score 21;	DB 6;	Length 48;	
Best Local Similarity	100.0%	Pred. No.	0.039;	Mismatches	0;
Matches	21;	Conservative	0;	Indels	0;
Qy	1 gtctgttcaggccctccaggaccc	21			
Db	10 GTCGTCAGCCTCCAGGACCC	30			

Tue Aug 27 15:49:52 2002

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Page 4

Db 10 GTCCTGGCACCCCTCCAGGCC 30

Search completed: August 26, 2002, 21:20:54
Job time: 7708 sec

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RESULT 2
AAH25408
ID AAH25408 standard; DNA; 21 BP.
XX
AC AAH25408;
XX
DT 22-AUG-2001 (first entry)
XX
DE Detection probe for a HCV DNA fragment.
XX
KW Magnetic glass particle; nucleic acid purification; probe; ss.
XX
OS Hepatitis C virus.
XX
FH Key modified base Location/Qualifiers
FT 1
FT /*tag= a
FT /note= "ruthenium3+-(tris-bipyridyl)-derivatisation"
XX WO200137291-A1.
PN
PD 25-MAY-2001.
XX
XX 17-NOV-2000; 2000WO-EP11459.
XX
PR 17-NOV-1999; 99EP-0122853.
PR 12-MAY-2000; 2000EP-0110165.
XX
PA (HOFF) ROCHE DIAGNOSTICS GMBH.
XX
PI Weindel K, Riedling M, Geiger A;
XX
DR WPI; 1994-151836/19.
XX
PT Anti-sense oligonucleotide(s) complementary to the hepatitis C virus genome - are useful as antiviral agents
XX
PS Claim 5; Page 70; 262pp; English.
XX
CC This oligonucleotide is an example of a preferred anti-sense compound i.e. it has a base sequence of 16-24 bases which is included within the 24 bases from G at position 127 to C at position 150 of AAQ6913 and which contains at least 16 bases from C at position 131 to A at position 146. The antisense oligonucleotide is useful for inhibiting translation of HCV genes.
CC
XX Sequence 22 BP; 3 A; 6 C; 10 G; 3 T; 0 other;
XX
PT Novel composition of magnetic glass particles for purification of DNA or RNA in automated processes
XX
PS Example 7; Page 96; 105pp; English.
XX
CC The specification describes a composition of magnetic glass particles, which contain at least one magnetic object with a mean diameter between 5-500 nm. The composition is useful for the purification of nucleic acids. The composition can be used to process large quantities of nucleic acid samples, because it does not involve the particles being centrifuged or the fluids being drawn through glass fiber filters. The present sequence represents a probe for a HCV DNA fragment. The DNA fragment can be purified using the method of the invention.
XX
SQ Sequence 21 BP; 3 A; 9 C; 6 G; 3 T; 0 other;

Query Match 100 %; Score 21; DB 22; Length 22;
Best Local Similarity 100 %; Pred. No. 0.076;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 4
AAQ64932/C
ID AAQ64932 standard; DNA; 22 BP.
XX
AC AAQ64932;
XX
DB 22 GTCCGCGCAGCTCCAGGACCC 2

RESULT 4
AAQ64932/C
ID AAQ64932 standard; DNA; 22 BP.
XX
AC AAQ64932;
XX
DB 22 GTCCGCGCAGCTCCAGGACCC 2

DE 19-DSC-1994 (first entry)
XX
Antisense Antisense oligonucleotide complementary to Hepatitis C Virus genome.
XX
KW Hepatitis C Virus; Non-A, non-B hepatitis virus; HCV; antisense; therapy; inhibition; viral protein precursor; ss.
XX
OS Synthetic.
XX
PN CA2104649-A.
XX
PD 26-FEB-1994.
XX
PP 23-AUG-1993; 93CA-2104649.
XX
PR 25-AUG-1992; 92JP-0248796.
PR 03-MAR-1993; 93JP-0042736.
XX
PA (SEKI/) SEKI M.
XX
PT Honda Y, Seki M, Yamada E;
XX
DR WPI; 1994-151836/19.

PT Anti-sense oligo:nucleotide(s) complementary to the hepatitis C virus genome - are useful as antiviral agents

PT

XX

PS Claim 5; Page 72; 262pp; English.

CC This oligonucleotide is an example of a preferred antisense compound i.e. it has a base sequence of 16-24 bases which is included within the 24 bases from G at position 127 to C at position 150 of AAQ6913 and which contains at least 16 bases from C at position 131 to A at position 146. The antisense oligonucleotide is useful for inhibiting translation of HCV genes.

XX

SQ Sequence 22 BP; 4 A; 6 C; 9 G; 3 T; 0 other;

Query Match 100 0%; Score 21; DB 15; Length 22; Best Local Similarity 100 0%; Pred. No. 0.076; Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 gtcgtgcagccctccaggaccc 21

Db 22 GTCGTGCAGCCTCCAGGACCC 2

RESULT 6

ID AAQ64937/C

ID AAQ64937 standard; DNA; 23 BP.

KW Hepatitis C Virus; Non-A, non-B hepatitis virus; HCV; antisense; therapy; inhibition; viral protein precursor; ss.

XX

AC AAQ64937;

XX

DT 19-DEC-1994 (first entry)

XX

DE Antisense oligonucleotide complementary to Hepatitis C Virus genome.

KW Hepatitis C Virus; Non-A, non-B hepatitis virus; HCV; antisense; therapy; inhibition; viral protein precursor; ss.

XX

OS Synthetic.

XX

PN CA2104649-A.

XX

PD 26-FEB-1994.

XX

PP 23-AUG-1993; 93CA-2104649.

XX

PR 25-AUG-1992; 92JP-0248796.

XX

PR 03-MAR-1993; 93JP-0042736.

XX

PA (SEKI/) SEKI M.

XX

PI Honda Y, Seki M, Yamada E;

XX

DR WPI; 1994-151866/19.

PT Anti-sense oligo:nucleotide(s) complementary to the hepatitis C virus genome - are useful as antiviral agents

XX

PS Claim 5; Page 74; 262pp; English.

CC This oligonucleotide is an example of a preferred antisense compound i.e. it has a base sequence of 16-24 bases which is included within the 24 bases from G at position 127 to C at position 150 of AAQ6913 and which contains at least 16 bases from C at position 131 to A at position 146. The antisense oligonucleotide is useful for inhibiting translation of HCV genes.

XX

SQ Sequence 23 BP; 4 A; 7 C; 9 G; 3 T; 0 other;

Query Match 100 0%; Score 21; DB 15; Length 23; Best Local Similarity 100 0%; Pred. No. 0.076; Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 gtcgtgcagccctccaggaccc 21

Db 21 GTCGTGCAGCCTCCAGGACCC 1

RESULT 7

ID AAQ64938/C

ID AAQ64938 standard; DNA; 24 BP.

KW Hepatitis C Virus; Non-A, non-B hepatitis virus; HCV; antisense; therapy; inhibition; viral protein precursor; ss.

XX

AC AAQ64938;

XX

DT 19-DEC-1994 (first entry)

XX

DE Antisense oligonucleotide complementary to Hepatitis C Virus genome.

KW Hepatitis C Virus; Non-A, non-B hepatitis virus; HCV; antisense; therapy; inhibition; viral protein precursor; ss.

XX

OS Synthetic.

Query Match 100 0%; Score 21; DB 15; Length 23; Best Local Similarity 100 0%; Pred. No. 0.076; Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX	CA2104649-A.	PS	Claim 5; Page 117; 262pp; English.
PN		XX	
XX		CC	This oligonucleotide is an example of a preferred antisense compound
PD	26-FEB-1994.	CC	i.e. it has a base sequence of 15-30 bases which is included
XX		CC	within the 49 bases from G at position 127 to C at position 175 of
PR	23-AUG-1993; 93CA-2104649.	CC	AAQ6913 and which contains at least 7 bases from C at position 147
XX		CC	to C at position 153. The antisense oligonucleotide is useful for
PR	25-AUG-1992; 92JP-0248796.	CC	Inhibiting translation of HCV genes.
PR	03-MAR-1993; 93JP-0042736.	XX	
PA	(SEKI/) SEKI M.	SQ	Sequence 25 BP; 3 A; 6 C; 13 G; 3 T; 0 other;
XX	Honda Y, Seki M, Yamada E;	PI	
XX		DR	WPI; 1994-151836/19.
PT	Anti-sense oligo:nucleotide(s) complementary to the hepatitis C	OY	1 9tcgtgcagctccggaccc 21
PT	virus genome - are useful as antiviral agents	Db	25 GTCGTGCAGCTCCAGGACCC 5
XX		Query Match	100 0%; Score 21; DB 15; Length 25;
XX		Best Local Similarity	100 0%; Pred. No. 0.076; 0; Mismatches
CC	Matches	Indels	0; Gaps 0;
CC		Gaps	0;
OY	1 9tcgtgcagctccggaccc 21	RESULT	9
Db	25 GTCGTGCAGCTCCAGGACCC 5	ID	AAQ6530/C
AAQ6530;	XX	ID	AAQ6530 standard; DNA; 26 BP.
AC	XX	XX	
XX		AC	AAQ6530;
DT	20-DEC-1994 (first entry)	XX	
DE	Antisense oligonucleotide complementary to Hepatitis C Virus genome.	DE	
XX		XX	
KW	Hepatitis C Virus; Non-A, non-B hepatitis virus; HCV; antisense;	XX	
KW	therapy; inhibition; viral protein precursor; ss.	XX	
OS	Synthetic.	OS	
XX		PN	CA2104649-A.
XX		PD	26-FEB-1994.
XX		XX	
XX		PR	25-AUG-1992; 92JP-0248796.
XX		PR	03-MAR-1993; 93JP-0042736.
XX		XX	
PA	(SEKI/) SEKI M.	PA	
XX	Honda Y, Seki M, Yamada E;	PI	
XX		DR	WPI; 1994-151836/19.
PT	Anti-sense oligo:nucleotide(s) complementary to the hepatitis C	OY	1 9tcgtgcagctccggaccc 21
PT	virus genome - are useful as antiviral agents	Db	25 GTCGTGCAGCTCCAGGACCC 5
XX		Query Match	100 0%; Score 21; DB 15; Length 26;
XX		Best Local Similarity	100 0%; Pred. No. 0.076; 0; Mismatches
CC	Matches	Indels	0; Gaps 0;
CC		Gaps	0;
OY	1 9tcgtgcagctccggaccc 21	RESULT	9
Db	25 GTCGTGCAGCTCCAGGACCC 5	ID	AAQ6530/C
AAQ6530;	XX	ID	AAQ6530 standard; DNA; 26 BP.
AC	XX	XX	
XX		AC	AAQ6530;
DT	20-DEC-1994 (first entry)	XX	
DE	Antisense oligonucleotide complementary to Hepatitis C Virus genome.	DE	
XX		XX	
KW	Hepatitis C Virus; Non-A, non-B hepatitis virus; HCV; antisense;	XX	
KW	therapy; inhibition; viral protein precursor; ss.	XX	
OS	Synthetic.	OS	
XX		PN	CA2104649-A.
XX		PD	26-FEB-1994.
XX		XX	
XX		PR	25-AUG-1992; 92JP-0248796.
XX		PR	03-MAR-1993; 93JP-0042736.
XX		XX	
PA	(SEKI/) SEKI M.	PA	
XX	Honda Y, Seki M, Yamada E;	PI	
XX		DR	WPI; 1994-151836/19.
PT	Anti-sense oligo:nucleotide(s) complementary to the hepatitis C	OY	1 9tcgtgcagctccggaccc 21
PT	virus genome - are useful as antiviral agents	Db	25 GTCGTGCAGCTCCAGGACCC 5
XX		Query Match	100 0%; Score 21; DB 15; Length 26;
XX		Best Local Similarity	100 0%; Pred. No. 0.076; 0; Mismatches
CC	Matches	Indels	0; Gaps 0;
CC		Gaps	0;
OY	1 9tcgtgcagctccggaccc 21	RESULT	9
Db	25 GTCGTGCAGCTCCAGGACCC 5	ID	AAQ6530/C
AAQ6530;	XX	ID	AAQ6530 standard; DNA; 26 BP.
AC	XX	XX	
XX		AC	AAQ6530;
DT	20-DEC-1994 (first entry)	XX	
DE	Antisense oligonucleotide complementary to Hepatitis C Virus genome.	DE	
XX		XX	
KW	Hepatitis C Virus; Non-A, non-B hepatitis virus; HCV; antisense;	XX	
KW	therapy; inhibition; viral protein precursor; ss.	XX	
OS	Synthetic.	OS	
XX		PN	CA2104649-A.
XX		PD	26-FEB-1994.
XX		XX	
XX		PR	25-AUG-1992; 92JP-0248796.
XX		PR	03-MAR-1993; 93JP-0042736.
XX		XX	
PA	(SEKI/) SEKI M.	PA	
XX	Honda Y, Seki M, Yamada E;	PI	
XX		DR	WPI; 1994-151836/19.
PT	Anti-sense oligo:nucleotide(s) complementary to the hepatitis C	OY	1 9tcgtgcagctccggaccc 21
PT	virus genome - are useful as antiviral agents	Db	25 GTCGTGCAGCTCCAGGACCC 5
XX		Query Match	100 0%; Score 21; DB 15; Length 26;
XX		Best Local Similarity	100 0%; Pred. No. 0.076; 0; Mismatches
CC	Matches	Indels	0; Gaps 0;
CC		Gaps	0;
OY	1 9tcgtgcagctccggaccc 21	RESULT	9
Db	25 GTCGTGCAGCTCCAGGACCC 5	ID	AAQ6530/C
AAQ6530;	XX	ID	AAQ6530 standard; DNA; 26 BP.
AC	XX	XX	
XX		AC	AAQ6530;
DT	20-DEC-1994 (first entry)	XX	
DE	Antisense oligonucleotide complementary to Hepatitis C Virus genome.	DE	
XX		XX	
KW	Hepatitis C Virus; Non-A, non-B hepatitis virus; HCV; antisense;	XX	
KW	therapy; inhibition; viral protein precursor; ss.	XX	
OS	Synthetic.	OS	
XX		PN	CA2104649-A.
XX		PD	26-FEB-1994.
XX		XX	
XX		PR	25-AUG-1992; 92JP-0248796.
XX		PR	03-MAR-1993; 93JP-0042736.
XX		XX	
PA	(SEKI/) SEKI M.	PA	
XX	Honda Y, Seki M, Yamada E;	PI	
XX		DR	WPI; 1994-151836/19.
PT	Anti-sense oligo:nucleotide(s) complementary to the hepatitis C	OY	1 9tcgtgcagctccggaccc 21
PT	virus genome - are useful as antiviral agents	Db	25 GTCGTGCAGCTCCAGGACCC 5

RESULT 10
 AAQ65036/C
 ID AAQ65036 standard; DNA; 26 BP.
 XX
 AC AAQ65036;
 XX
 DT 20-DEC-1994 (first entry)
 XX
 DE Antisense oligonucleotide complementary to Hepatitis C Virus genome.
 KW Hepatitis C Virus; Non-A, non-B hepatitis virus; HCV; antisense;
 KW therapy; inhibition; viral protein precursor; ss.
 OS Synthetic.
 XX
 PN CA2104649-A.

XX
 PD 26-FEB-1994.
 XX
 PF 23-AUG-1993; 93CA-2104649.
 XX
 PR 25-AUG-1992; 92JP-0248796.
 PR 03-MAR-1993; 93JP-0042736.
 XX
 PA (SEKI/) SEKI M.
 XX
 PI Honda Y, Seki M, Yamada E;
 XX
 DR WPI; 1994-151836/19.
 XX
 CC Anti:sense oligo:nucleotide(s) complementary to the hepatitis C
 PT virus genome - are useful as antiviral agents
 XX
 PS Claim 5; Page 113; 262pp; English.
 XX
 CC This oligonucleotide is an example of a preferred antisense compound
 i.e. It has a base sequence of 15-30 bases which is included
 CC within the 49 bases from G at position 127 to C at position 175 of
 CC AAQ64913 and which contains at least 7 bases from C at position 147
 CC to C at position 153. The antisense oligonucleotide is useful for
 CC inhibiting translation of HCV genes.
 XX
 SQ Sequence 27 BP; 4 A; 7 C; 13 G; 3 T; 0 other;
 XX
 DR Best Local Similarity 100%; Score 21; DB 15; Length 27;
 XX
 CC Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 CC
 PT virus genome - are useful as antiviral agents
 XX
 PS Claim 5; Page 117; 262pp; English.
 XX
 CC This oligonucleotide is an example of a preferred antisense compound
 i.e. It has a base sequence of 15-30 bases which is included
 CC within the 49 bases from G at position 127 to C at position 175 of
 CC AAQ64913 and which contains at least 7 bases from C at position 147
 CC to C at position 153. The antisense oligonucleotide is useful for
 CC inhibiting translation of HCV genes.
 XX
 SQ Sequence 27 BP; 4 A; 7 C; 13 G; 3 T; 0 other;

Query Match 100%; Score 21; DB 15; Length 27;
 Best Local Similarity 100%; Pred. No. 0.076; Mismatches 0; Indels 0; Gaps 0;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 QY 1 gtgcgtgcagctccaggacc 21
 ||||| ||||| |||||
 DB 26 GTCGTCAGCTCCAGGACC 6

RESULT 11
 AAQ65026/C
 ID AAQ65026 standard; DNA; 27 BP.
 XX
 AC AAQ65026;
 XX
 DT 20-DEC-1994 (first entry)
 XX
 DE Antisense oligonucleotide complementary to Hepatitis C Virus genome.
 KW Hepatitis C Virus; Non-A, non-B hepatitis virus; HCV; antisense;
 KW therapy; inhibition; viral protein precursor; ss.
 OS Synthetic.
 XX
 PN CA2104649-A.

XX
 PD 26-FEB-1994.
 XX
 PF 23-AUG-1993; 93CA-2104649.
 XX
 PR 25-AUG-1992; 92JP-0248796.
 PR 03-MAR-1993; 93JP-0042736.
 XX
 PA (SEKI/) SEKI M.
 XX
 PI Honda Y, Seki M, Yamada E;
 XX
 DR WPI; 1994-151836/19.
 XX
 CC Anti:sense oligo:nucleotide(s) complementary to the hepatitis C
 PT virus genome - are useful as antiviral agents
 XX
 PS Claim 5; Page 115; 262pp; English.
 XX
 CC This oligonucleotide is an example of a preferred antisense compound

1.e. it has a base sequence of 15-30 bases which is included within the 49 bases from G at position 127 to C at position 175 of AAQ4913 and which contains at least 7 bases from C at position 147 to C at position 153. The antisense oligonucleotide is useful for inhibiting translation of HCV genes.

SQ sequence 27 BP; 5 A; 6 C; 13 G; 3 T; 0 other;

Query Match 100.0%; Score 21; DB 15; Length 27;
Best Local Similarity 100.0%; Pred. No. 0.075; Mismatches 0; Indels 0; Gaps 0;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 gtcgtgcagccgtccaggaccc 21
Db 26 GTCCGTGCAGCCTCCAGGACCC 6

RESULT 13

AAQ5037/C

ID AAQ5037 standard; DNA; 27 BP.

XX AAQ5037; Hepatitis C virus.

XX AC AAQ5037; Hepatitis C virus.

XX XX

XX DT 08-JAN-2001 (first entry)

XX DE HCV probe C96-22-PRB.

XX KW Hepatitis C virus; HCV; HCV detection; probe; ss.

XX OS Hepatitis C virus.

XX PN EP1026262-A2.

XX DD 09-AUG-2000.

XX PR 01-FEB-2000; 2000EP-0300763.

XX PR 03-FEB-1999; 99US-0118497.

XX PA (ORTHO) ORTHO CLINICAL DIAGNOSTICS INC.

XX PI Linnen JM, Gorman KM;

XX DR WPI; 2000-507254/46.

XX PT Detecting hepatitis C virus in biological sample involves amplifying reverse transcribed products of virus RNA using amplification primers whose sequences correspond to 5' or 3' non-coding region of the virus RNA.

XX PT

XX PS Claim 30; Page 27; 28PP; English.

XX CC The present sequence is a probe used in a method for detecting hepatitis C virus (HCV) RNA in biological samples. The HCV RNA is reverse transcribed to generate cDNA. This is then amplified with primers corresponding to the 5' or 3' non-coding region of HCV. The product was captured by hybridisation to oligonucleotide probes, including the present sequence, which were covalently attached to latex particles and deposited on the surface of a flow through membrane. The probe/product complex was reacted with streptavidin horseradish peroxidase conjugate, which catalyses the oxidative conversion of a dye precursor to a blue dye. The method is useful for the diagnosis of HCV infection in patients, in testing the efficacy of anti-HCV therapeutic regimes, and in screening blood for HCV-infected samples. The method provides an improved single-round, reverse transcription/amplicification assay which detects low copy levels of HCV RNA. The primers and assay system are designed to allow the co-amplification of multiple regions of the HCV genome, multiple viral species, and an internal positive control (IPC) RNA (or DNA). Simultaneous amplification/detection of multiple regions of the HCV genome increases assay sensitivity and the co-amplification of an IPC decreases the likelihood of false negative results because of PCR inhibition.

XX SQ Sequence 27 BP; 5 A; 8 C; 9 G; 5 T; 0 other;

Query Match 100.0%; Score 21; DB 15; Length 27;
Best Local Similarity 100.0%; Pred. No. 0.075; Mismatches 0; Indels 0; Gaps 0;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 gtcgtgcagccgtccaggaccc 21
Db 27 GTCCGTGCAGCCTCCAGGACCC 7

RESULT 15

AAQ5038/C

ID AAQ5038 standard; DNA; 28 BP.

XX AAQ5038; Hepatitis C virus.

XX AC AAQ5038; Hepatitis C virus.

XX XX

RESULT 14

Query Match, 100.0%; Score 21; DB 15; Length 28;
 Best Local Similarity 100.0%; Pred. No. 0.075; Mismatches 0; Indels 0; Gaps 0;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 gtctgtgcgcctcaggacc 21
 ||||||| 7

Db 27 GTCGTGCAGCCCTCAGGACCC 7

RESULT 18
 AAQ65039/c
 ID AAQ65039 standard; DNA; 29 BP.
 XX
 AC AAQ65039;
 XX
 DT 20-DEC-1994 (first entry)
 XX
 DE Antisense oligonucleotide complementary to Hepatitis C Virus genome.
 XX
 KW Hepatitis C Virus; Non-A, non-B hepatitis virus; HCV; antisense;
 KW therapy; inhibition; viral protein precursor; ss.
 XX
 OS Synthetic.

XX
 PN CA2104649-A.
 PR 25-AUG-1992; 92JP-024896.
 PR 03-MAR-1993; 93JP-0042736.
 XX
 PD 26-FEB-1994.
 XX
 PF 23-AUG-1993; 93CA-2104649.
 XX
 PR 25-AUG-1992; 92JP-024896.
 PR 03-MAR-1993; 93JP-0042736.
 XX
 PA (SEKI/) SEKI M.
 XX
 PI Honda Y, Seki M, Yamada E;
 XX
 DR WPI; 1994-151836/19.
 XX
 PN CA2104649-A.
 XX
 PD 26-FEB-1994.
 XX
 PR 23-AUG-1993; 93CA-2104649.
 XX
 PT Anti:sense oligo:nucleotide(s) complementary to the hepatitis C
 PT virus genome - are useful as antiviral agents
 XX
 PS claim 5; Page 114; 262pp; English.
 XX
 CC This oligonucleotide is an example of a preferred antisense compound
 CC i.e. it has a base sequence of 15-30 bases which is included
 CC within the 49 bases from G at position 127 to C at position 175 of
 CC AAQ64913 and which contains at least 7 bases from C at position 147
 CC to C at position 153. The antisense oligonucleotide is useful for
 CC inhibiting translation of HCV genes.
 XX
 SQ Sequence 29 BP; 5 A; 7 C; 14 G; 3 T; 0 other;

Query Match, 100.0%; Score 21; DB 15; Length 29;
 Best Local Similarity 100.0%; Pred. No. 0.075; Mismatches 0; Indels 0; Gaps 0;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 gtctgtgcgcctcaggacc 21
 ||||||| 7

Db 27 GTCGTGCAGCCCTCAGGACCC 7

RESULT 20
 AAQ65033/c
 ID AAQ65033 standard; DNA; 29 BP.
 XX
 AC AAQ65033;
 XX
 DT 20-DEC-1994 (first entry)
 XX
 DE Antisense oligonucleotide complementary to Hepatitis C Virus genome.
 XX
 KW Hepatitis C Virus; Non-A, non-B hepatitis virus; HCV; antisense;
 KW therapy; inhibition; viral protein precursor; ss.
 XX
 OS Synthetic.

XX
 PN CA2104649-A.
 XX
 PR 25-AUG-1992; 92JP-024896.
 PR 03-MAR-1993; 93JP-0042736.
 XX
 PA (SEKI/) SEKI M.
 XX
 PI Honda Y, Seki M, Yamada E;
 XX
 DE Antisense oligonucleotide complementary to Hepatitis C Virus genome.

RESULT 19
 AAQ65028/c
 ID AAQ65028 standard; DNA; 29 BP.
 XX
 AC AAQ65028;
 XX
 DT 20-DEC-1994 (first entry)
 XX
 DE Antisense oligonucleotide complementary to Hepatitis C Virus genome.

XX
OS Synthetic.
XX
PN CA2104649-A.
XX
PD 26-FEB-1994.
XX
PF 23-AUG-1993; 93CA-2104649.
XX
PR 25-AUG-1992; 92JP-0248796.
PR 03-MAR-1993; 93JP-0042736.
XX
PA (SEKI-) SEKI M.
XX
PI Honda Y, Seki M, Yamada E;
XX
DR WPI; 1994-151836/19.
XX
PT Anti-sense oligo:nucleotide(s) complementary to the hepatitis C virus genome - are useful as antiviral agents
XX
PS Claim 5; Page 116; 262pp; English.
XX
CC This oligonucleotide is an example of a preferred antisense compound i.e. it has a base sequence of 15-30 bases which is included within the 49 bases from G at position 175 to C at position 177 to AA06913 and which contains at least 7 bases from C at position 147 to C at position 153. The antisense oligonucleotide is useful for inhibiting translation of HCV genes.
XX
SQ Sequence 30 BP; 5 A; 6 C; 16 G; 3 T; 0 other;
Query Match 100.0%; Score 21; DB 15; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.075; Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 gtcggtcagctccaggaccc 21
Db 29 GTCGGTCAGCTCCAGGACCC 9

RESULT 24
AAZ23541
ID AAZ23541 standard; DNA; 48 BP.
XX
AC AAZ23541;
XX
DT 21-DEC-1999 (first entry)
XX
DE Human DNA fragment 1.
XX
KW Assay; amplification; hybridisation; probe; detection; viral; bacterial;
XX
OS Homo sapiens.
XX
PN DE19914828-A1.
XX
PD 07-OCT-1999.
XX
PF 02-APR-1998; 98DE-1014828.
XX
PR 02-APR-1998; 98DE-1014828.
XX
PA (HOFF) ROCHE DIAGNOSTICS GMBH.
PI Kessler C, Haberhausen G, Batz H, Oerum H;
XX
DR WPI; 1999-552286/47.
XX
PT Nucleic acid amplification assay for detecting viral, bacterial, cellular, yeast or fungal nucleic acids
XX
PS Disclosure; Fig 4; 28pp; German.
XX
CC This invention describes a novel assay for a nucleic acid comprises:
CC (a) generating amplification products from a fragment of the nucleic acid;
CC (b) contacting the amplification products with a probe; and
CC (c) detecting hybridization between the amplification product and the probe. The assay is useful for detection of viral, bacterial, cellular, yeast or fungal nucleic acids in human, animal, bacterial, plant, yeast or fungal samples, e.g. feces, smears, cell suspensions, cultures or tissue, cell or liquid biopsy samples. This sequence represents a fragment of the human genome which is used in the method of the invention.
XX
SQ Sequence 48 BP; 9 A; 17 C; 14 G; 8 T; 0 other;

XX
PS Disclosure; Fig 4; 28pp; German.
XX
CC This invention describes a novel assay for a nucleic acid comprises:
CC (a) generating amplification products from a fragment of the nucleic acid;
CC (b) contacting the amplification products with a probe; and
CC (c) detecting hybridization between the amplification product and the probe. The assay is useful for detection of viral, bacterial, cellular, yeast or fungal nucleic acids in human, animal, bacterial, plant, yeast or fungal samples, e.g. feces, smears, cell suspensions, cultures or tissue, cell or liquid biopsy samples. This sequence represents a fragment of the HCV genome used in the method of the invention.

Tue Aug 27 15:49:54 2002

us-10-037-990a-3.oli.rng

Page 11

Query Match 100.0%; Score 21; DB 20; Length 48;
Best Local Similarity 100.0%; Pred. No. 0.072;
Matches 21; Conservative 0; Mismatches 0; Indels 0;
Gaps 0;

Qy 1 gtctgtgcaggccctcaggaccc 21
|||||||
Db 10 gtctgtgcaggccctcaggaccc 30

Search completed: August 26, 2002, 22:24:56
Job time: 6235 sec

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GenCore version 4.5
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OM nucleic - nucleic search, using sw model
Run on: August 26, 2002, 20:38:47 ; Search time 119.4 Seconds
(without alignments)

Title: US-10-037-990a-1
Perfect score: 24
Sequence: 1 gcagaaaggcttagccatggcgt 24
Scoring table: OLIGO_NUC_Gapop_60.0 , Gapext 60.0

Searched: 383533 seqs, 122816752 residues

Word size : 21
Total number of hits satisfying chosen parameters: 20
Minimum DB seq length: 0
Maximum DB seq length: 100

Post-processing: Listing first 65 summaries

Database : Issued_Patents_NA:*

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4: /cggn2_6/ptodata/2/ina/6B_COMB_seq:*
5: /cggn2_6/ptodata/2/ina/PCNUS_COMB_seq:*
6: /cggn2_6/ptodata/2/ina/backfileseq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	24	100.0	24	1 US-08-240-547-5
2	24	100.0	24	1 US-08-449-050-17
3	24	100.0	24	1 US-08-332-616A-9
4	24	100.0	24	1 US-08-317-220-9
5	24	100.0	24	1 US-08-675-153-7
6	24	100.0	24	2 US-08-338-920-4
7	24	100.0	24	2 US-08-441-253-7
8	24	100.0	24	2 US-08-881-551-7
9	24	100.0	24	4 US-09-282-054-7
10	26	100.0	26	1 US-08-240-547-6
11	24	100.0	26	2 US-09-738-928-1
12	24	100.0	26	3 US-09-039-865-3
13	23	95.8	3	US-09-078-220A-9
14	23	95.8	37	PTC-US94-0507-14
15	23	95.8	58	PTC-US94-0540-12
16	21	87.5	21	4 US-09-034-205-25
17	21	87.5	21	4 US-09-934-097A-25
18	21	87.5	21	4 US-08-851-588-25
19	21	87.5	21	4 US-09-677-218B-25
20	21	87.5	21	4 US-09-677-192-25

RESULT 1
US-08-240-547-5

ALIGNMENTS

Sequence 5, Application US/08240547
Patent No. 5526669
GENERAL INFORMATION:
APPLICANT: Resnick, Robert M.
APPLICANT: Young, Karen K.Y.
TITLE OF INVENTION: Primers and Probes for detection of Hepatitis C and No. 552669el variants
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hoffmann-La Roche Inc.
STREET: 340 Kingsland Street
CITY: Nutley
STATE: NJ
ZIP: 07110-1199
COMPUTER READABLE FORM:
MEDIM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/240,547
FILING DATE:
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US/07/918,844
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: SLAS Ph.D., Stacey R.
REGISTRATION NUMBER: 32,630
REFERENCE/DOCKET NUMBER: 8586
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 814-8863
TELEFAX: (510) 814-2977
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 base Pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-240-547-5

Query Match Best Local Similarity 100.0%; Score 24; DB 1; Length 24;
Matches 24; Conservative 100.0%; Pred. No. 1.8e+05; Mismatches 0; Indels 0; Gaps 0;

Qy 1 gcagaaaggcttagccatggcgt 24
Db 1 GCAGAAAGCGCTAGCCATGGCGT 24

GENERAL INFORMATION:
APPLICANT: Geiland, David
APPLICANT: Myers, Thomas
APPLICANT: Myers, Christopher
TITLE OF INVENTION: Reagents and Methods for Coupled High Temperature Reverse Transcription and Polymerase Chain Reaction
TITLE OF INVENTION: Reactions
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hoffmann-La Roche Inc.
STREET: 340 Kingsland Street
CITY: Nutley
STATE: New Jersey
COUNTRY: U.S.A.
ZIP: 07110
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/449,050
 FILING DATE:
 CLASSIFICATION: 435
 INFORMATION FOR SEQ ID NO: 17:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 24 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLogy: linear
 MOLECULE TYPE: genomic DNA
 US-08-449-050-17

Query Match 100.0%; Score 24; DB 1; Length 24;
 Best Local Similarity 100.0%; Pred. No. 1.8e-05;
 Matches 24; Conservative 0; Mismatches 0;
 Indels 0; Gaps 0;

Qy 1 9cagaaggcttacccatgcgt 24
 Db 1 GCAGAAGCGCTAGCCATGGGT 24

RESULT 4
 US-08-317-220-9
 ; Sequence 9, Application US/08317220
 ; Patent No. 5654179
 GENERAL INFORMATION:
 APPLICANT: LIN, LILY
 TITLE OF INVENTION: NUCLEAR ACID PREPARATION METHODS
 NUMBER OF SEQUENCES: 14
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: PETER G. CARROLL
 STREET: 220 Montgomery Street, Suite 2200
 CITY: San Francisco
 STATE: California
 COUNTRY: United States of America
 ZIP: 94104

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/317,220
 FILING DATE:
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/08/044,649
 FILING DATE:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/901,545
 FILING DATE: 19-JUN-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/614,921
 FILING DATE: 14-NOV-1990
 ATTORNEY/AGENT INFORMATION:
 NAME: CARROLL, PETER G.
 REGISTRATION NUMBER: 32,837
 REFERENCE/DOCKET NUMBER: HRI-00542
 TELEPHONE: (415) 705-9410
 TELEFAX: (415) 397-8338
 INFORMATION FOR SEQ ID NO: 9:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 24 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLogy: linear
 MOLECULE TYPE: DNA (genomic)
 US-08-317-220-9

RESULT 5
 US-08-675-153-7
 ; Sequence 7, Application US/08675153
 ; Patent No. 567124
 GENERAL INFORMATION:

APPLICANT: Dubois, Dwight
 APPLICANT: Winkler, Matthew
 APPLICANT: Pasloske, Brittan L.
 TITLE OF INVENTION: RIBONUCLEASE RESISTANT VIRAL
 NUMBER OF SEQUENCES: 8
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Arnold, White & Durkee
 STREET: P.O. Box 4433
 CITY: Houston
 STATE: Texas
 COUNTRY: United States of America
 ZIP: 77210
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/675,153
 FILING DATE: Concurrently Herewith
 CLASSIFICATION: 530
 ATTORNEY/AGENT INFORMATION:
 NAME: Wilson, Mark B.
 REGISTRATION NUMBER: 37,259
 REFERENCE/DOCKET NUMBER: AMBI:026
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (512) 418-3000
 TELEFAX: (512) 474-7577
 INFORMATION FOR SEQ ID NO: 7:
 SEQUENCE CHARACTERISTICS:
 SEQUENCE: CTCGCTTGGCGATGGCGT
 LENGTH: 24 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLogy: linear
 MOLECULE TYPE: DNA (genomic)
 US-08-738-928-4

RESULT 6
 US-08-738-928-4
 Sequence 4, Application US/08738928
 Patent No. 5837442
 GENERAL INFORMATION:
 APPLICANT: Tsang, Sue Y.
 TITLE OF INVENTION: Oligonucleotide Primers for Amplifying
 TITLE OF INVENTION: HCV Nucleic Acid
 NUMBER OF SEQUENCES: 5
 CORRESPONDENCE ADDRESS:
 ADDRESSEEE: Hoffmann-La Roche Inc.
 STREET: 340 Kingsland Street
 CITY: Nutley
 STATE: NJ
 COUNTRY: U.S.A.
 ZIP: 07110
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US 5,677,124
 FILING DATE: 03-JUL-1996
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 5,677,124
 FILING DATE: 03-JUL-1996
 ATTORNEY/AGENT INFORMATION:
 NAME: WILSON, MARK B.
 REGISTRATION NUMBER: 37,259
 REFERENCE/DOCKET NUMBER: AMBI:026-1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (512) 418-3000
 TELEFAX: (512) 474-7577
 INFORMATION FOR SEQ ID NO: 7:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 24 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLogy: linear
 MOLECULE TYPE: DNA (genomic)
 US-08-841-252-7

Query Match 100.0%; Score 24; DB 1; Length 24;
 Best Local Similarity 100.0%; Pred. No. 1.8e-05;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 gcagaagaagcttcgtggatcgctg 24
 Db 1 GCAGAAAGCGCTAGCCATGGCGT 24

RESULT 7
 US-08-841-252-7
 Sequence 7, Application US/08841252
 Patent No. 5919625
 GENERAL INFORMATION:
 APPLICANT: DUBOIS, DWIGHT
 APPLICANT: WINKLER, MATTHEW
 APPLICANT: PASLOSKA, BRITTAN L.
 TITLE OF INVENTION: RIBONUCLEASE RESISTANT VIRAL RNA
 NUMBER OF SEQUENCES: 8
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: ARNOLD WHITE & DURKEE
 STREET: P.O. BOX 4433
 CITY: HOUSTON
 STATE: TEXAS
 COUNTRY: USA
 ZIP: 77210
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/841,252
 FILING DATE: 29-APR-1997
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 5,677,124
 FILING DATE: 03-JUL-1996
 ATTORNEY/AGENT INFORMATION:
 NAME: WILSON, MARK B.
 REGISTRATION NUMBER: 37,259
 REFERENCE/DOCKET NUMBER: AMBI:026-1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (512) 418-3000
 TELEFAX: (512) 474-7577
 INFORMATION FOR SEQ ID NO: 7:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 24 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLogy: linear
 MOLECULE TYPE: DNA (genomic)
 US-08-841-252-7

Query Match 100.0%; Score 24; DB 2; Length 24;
 Best Local Similarity 100.0%; Pred. No. 1.8e-05;

Matches	Conservative	Mismatches	Indels	Caps	O;
RESULT 8	0;	0;	0;	0;	0;
US-08-881-571-7					
Sequence 7, Application US/08881571					
Patent No. 593262					
GENERAL INFORMATION:					
APPLICANT: Pasloske, Brittan L.					
APPLICANT: Dubois, Dwight					
APPLICANT: Brown, David					
TITLE OF INVENTION: RIBONUCLEASE RESISTANT RNA PREPARATION					
TITLE OF INVENTION: AND UTILIZATION					
NUMBER OF SEQUENCES: 8					
CORRESPONDENCE ADDRESS:					
ADDRESSEE: Arnold, White & Durkee					
STREET: P.O. Box 4433					
CITY: Houston					
STATE: Texas					
COUNTRY: USA					
ZIP: 77210					
COMPUTER READABLE FORM:					
MEDIUM TYPE: Floppy disk					
COMPUTER: IBM PC compatible					
OPERATING SYSTEM: PC-DOS/MS-DOS					
SOFTWARE: PatentIn Release #1.0, Version #1.30					
CURRENT APPLICATION DATA:					
APPLICATION NUMBER: US/08/881,571					
FILING DATE: Concurrently Herewith					
CLASSIFICATION: 435					
PRIOR APPLICATION DATA:					
APPLICATION NUMBER: US 08/675,153					
FILING DATE: 03-JUL-1996					
PRIOR APPLICATION DATA:					
APPLICATION NUMBER: US 60/021,145					
FILING DATE: 03-JUL-1996					
ATTORNEY/AGENT INFORMATION:					
NAME: Wilson, Mark B.					
REFERENCE/DOCKET NUMBER: AMBI:033					
TELECOMMUNICATION INFORMATION:					
TELEPHONE: 512/418-3000					
TELEFAX: 512/474-7577					
INFORMATION FOR SEQ ID NO: 7:					
SEQUENCE CHARACTERISTICS:					
LENGTH: 24 base pairs					
TYPE: nucleic acid					
STRANDEDNESS: single					
TOPOLOGY: linear					
US-08-881-571-7					
RESULT 9					
US-09-282-054-7					
Query Match 100.0%; Score 24; DB 2; Length 24;					
Best Local Similarity 100.0%; Pred. No. 1.8e-05; Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
QY 1 ggccaaaggcttcaggcatggcgt 24					
DB 1 GCAGAAAGCGCTAGCCATGGCGT 24					
RESULT 9					
US-09-282-054-7					
Sequence 6, Application US/08240547					
Patent No. 5527669					
GENERAL INFORMATION:					
APPLICANT: Resnick, Robert M.					
APPLICANT: Young, Karen K.Y.					
APPLICANT: Primers and Probes for Detection of Hepatitis C and No. 5527669el Variants					
NUMBER OF SEQUENCES: 43					
CORRESPONDENCE ADDRESS:					
ADDRESSEE: Hoffmann-La Roche Inc.					
STREET: 340 Kingsland Street					
CITY: Nutley					
STATE: NJ					
COUNTRY: U.S.A.					
ZIP: 07110-1199					
COMPUTER READABLE FORM:					
MEDIUM TYPE: Floppy disk					

COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/240,547
 FILING DATE:
 CLASSIFICATION: 435
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US/07/918,844
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Sias, Ph.D., Stacey R.
 REGISTRATION NUMBER: 32,630
 REFERENCE/DOCKET NUMBER: 8586
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (510) 814-2977
 TELEFAX: (510) 814-2963
 INFORMATION FOR SEQ ID NO: 6:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 26 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 US-08-240-547-6

RESULT 11
 Query Match 100.0%; Score 24; DB 1; Length 26;
 Best Local Similarity 100.0%; Pred. No. 1.8e-05; Mismatches 0; Indels 0; Gaps 0;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 gcagaagcgcttaaccatggcgt 24
 Db 3 GCAGAAAGCGCTAGCCATGGCGT 26

US-08-738-928-1
 Sequence 1, Application US/08738928
 PATENT NO. 5537442
 GENERAL INFORMATION:
 APPLICANT: Tsang, Sue Y.
 TITLE OF INVENTION: Oligonucleotide Primers for Amplifying
 TITLE OF INVENTION: HCV Nucleic Acid
 NUMBER OF SEQUENCES: 5
 CORRESPONDENCE ADDRESS:
 ADDRESS: Hoffmann-La Roche Inc.
 STREET: 340 Kingsland Street
 CITY: Nutley
 STATE: NJ
 COUNTRY: U.S.A.
 ZIP: 07110

COMPUTER READABLE FORM:
 MEDIUM TYPE: floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/039,866
 FILING DATE:
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: Petty, Douglas A.
 REGISTRATION NUMBER: 35,321
 REFERENCE/DOCKET NUMBER: 1023P
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 26 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 US-09-039-866-3

RESULT 13
 Query Match 100.0%; Score 24; DB 3; Length 26;
 Best Local Similarity 100.0%; Pred. No. 1.8e-05; Mismatches 0; Indels 0; Gaps 0;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 gcagaagcgcttaaccatggcgt 24
 Db 1 GCAGAAAGCGCTAGCCATGGCGT 24

US-09-078-290A-9
 Sequence 9, Application US/09078290A
 PATENT NO. 6048696
 GENERAL INFORMATION:
 APPLICANT: Hoffman, Leslie M.
 APPLICANT: Hawkins, Gregory A.
 TITLE OF INVENTION: METHOD FOR IDENTIFYING NUCLEIC ACID MOLECULES
 NUMBER OF SEQUENCES: 12
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Quarles & Brady

INFORMATION FOR SEQ ID NO: 1:
 TELEPHONE: (510) 814-2974
 TELEFAX: (510) 814-2977
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 26 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single

STREET: 411 East Wisconsin Avenue
 CITY: Milwaukee
 STATE: Wisconsin
 COUNTRY: U.S.A.
 ZIP: 53202-4497
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/078-290A
 FILING DATE:
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Baker, Jean C.
 REGISTRATION NUMBER: 35,433
 REFERENCE/DOCKET NUMBER: 310307.90100
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (414) 277-5709
 TELEFAX: (414) 271-3552
 INFORMATION FOR SEQ ID NO: 9:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 24 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: Oligonucleotide
 US-09-078-290A-9

Query Match 95.8%; Score 23; DB 3; Length 24;
 Best Local Similarity 100.0%; Pred. No. 6.9e-05; Mismatches 0; Indels 0; Gaps 0;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 2 cagaaaagcqtcataccatggcgt 24
 Db 1 CAGAAAGCGCTAGCCATGGGT 23

RESULT 14
 PCT-US94-05407-14
 Sequence 14, Application PC/US9405407
 GENERAL INFORMATION:
 APPLICANT:
 TITLE OF INVENTION: "NUCLEIC ACID TAGGED IMMUNOASSAY"
 NUMBER OF SEQUENCES: 14
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: NEEDLE & ROSENBERG, P.C.
 STREET: Suite 1200, 127 Peachtree Street
 CITY: Atlanta
 STATE: Georgia
 COUNTRY: USA
 ZIP: 30303
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/US94/05407
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: 08/061,694
 FILING DATE: 13-MAY-1993
 INFORMATION FOR SEQ ID NO: 12:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 58 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: oligonucleotide
 PCT-US94-05407-12

Query Match 95.8%; Score 23; DB 5; Length 37;
 Best Local Similarity 100.0%; Pred. No. 6.7e-05; Mismatches 0; Indels 0; Gaps 0;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 2 cagaaaagcqtcataccatggcgt 24
 Db 14 CAGAAAGCGCTAGCCATGGGT 36

RESULT 15
 PCT-US94-05407-12
 Sequence 12, Application PC/US9405407
 GENERAL INFORMATION:
 APPLICANT:
 TITLE OF INVENTION: "NUCLEIC ACID TAGGED IMMUNOASSAY"
 NUMBER OF SEQUENCES: 14
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: NEEDLE & ROSENBERG, P.C.
 STREET: Suite 1200, 127 Peachtree Street
 CITY: Atlanta
 STATE: Georgia
 COUNTRY: USA
 ZIP: 30303
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/US94/05407
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: 08/061,694
 FILING DATE: 13-MAY-1993
 INFORMATION FOR SEQ ID NO: 12:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 58 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: oligonucleotide
 PCT-US94-05407-12

Query Match 95.8%; Score 23; DB 5; Length 37;
 Best Local Similarity 100.0%; Pred. No. 6.7e-05; Mismatches 0; Indels 0; Gaps 0;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 cagaaaagcqtcataccatggcgt 24
 Db 14 CAGAAAGCGCTAGCCATGGGT 36

RESULT 16
 US-09-034-205-25
 Sequence 25, Application US/09034205
 Patent No. 619419
 GENERAL INFORMATION:
 APPLICANT: Lymichev, Victor I.
 APPLICANT: Brow, Mary Ann D.
 APPLICANT: Fors, Lance
 APPLICANT: Neri, Bruce P.
 TITLE OF INVENTION: TARGET-DEPENDENT REACTIONS USING
 TITLE OF INVENTION: STRUCTURE-BRIDGING OLIGONUCLEOTIDES
 NUMBER OF SEQUENCES: 68
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: MEDLEN & CARROLL, LLP
 STREET: 220 Montgomery Street, Suite 2200
 CITY: San Francisco
 STATE: CA
 COUNTRY: USA
 ZIP: 94104
 COMPUTER READABLE FORM:

Query Match 95.8%; Score 23; DB 5; Length 37;
 Best Local Similarity 100.0%; Pred. No. 6.7e-05; Mismatches 0; Indels 0; Gaps 0;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 cagaaaagcqtcataccatggcgt 24
 Db 14 CAGAAAGCGCTAGCCATGGGT 36

RESULT 17
 US-09-034-205-25
 Sequence 25, Application US/09034205
 Patent No. 619419
 GENERAL INFORMATION:
 APPLICANT: Lymichev, Victor I.
 APPLICANT: Brow, Mary Ann D.
 APPLICANT: Fors, Lance
 APPLICANT: Neri, Bruce P.
 TITLE OF INVENTION: TARGET-DEPENDENT REACTIONS USING
 TITLE OF INVENTION: STRUCTURE-BRIDGING OLIGONUCLEOTIDES
 NUMBER OF SEQUENCES: 68
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: MEDLEN & CARROLL, LLP
 STREET: 220 Montgomery Street, Suite 2200
 CITY: San Francisco
 STATE: CA
 COUNTRY: USA
 ZIP: 94104
 COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/034,205
 FILING DATE:
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: Macknight, Kamrin T.
 REGISTRATION NUMBER: 38,230
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 705-8410
 TELEFAX: (415) 397-8338
 INFORMATION FOR SEQ ID NO: 25:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 21 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 MOLECULE TYPE: other nucleic acid
 DESCRIPTION: /desc = "DNA"
 US-09-034-205-25

RESULT 17
 US-08-934-097A-25
 Sequence 25, Application US/08934097A
 Patient No. 6210880
 GENERAL INFORMATION:
 APPLICANT: Lymichev, Victor I.
 APPLICANT: Brown, Mary Ann D.
 APPLICANT: Fors, Lance
 APPLICANT: Neri, Bruce P.
 TITLE OF INVENTION: Polymorphism Analysis By Nucleic Acid
 TITLE OF INVENTION: Structure Probing With Structure-Bridging
 NUMBER OF SEQUENCES: 51
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: MEDLEN & CARROLL, LLP
 STREET: 220 Montgomery Street, Suite 2200
 CITY: San Francisco
 STATE: CA
 COUNTRY: USA
 ZIP: 94104
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/851,588
 FILING DATE:
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Ingolia, Diane E.
 REGISTRATION NUMBER: 40,027
 REFERENCE/DOCKET NUMBER: FORS-02277
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 705-8410
 TELEFAX: (415) 397-8338
 INFORMATION FOR SEQ ID NO: 25:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 21 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 MOLECULE TYPE: other nucleic acid
 DESCRIPTION: /desc = "DNA"
 US-08-851-588-25

Query Match 87.5%; Score 21; DB 4; Length 21;
 Best Local Similarity 100.0%; Pred. No. 0.00099; Mismatches 0; Indels 0; Gaps 0;
 Matches 21; Conservative 0; MisMatch 0; Indel 0;

QY 1 gcagaaaaggcttacccatgg 21
 DB 1 GCAGAAAGCGCTAGCCATGG 21

RESULT 18
 US-08-851-588-25
 Sequence 25, Application US/08851588
 Patient No. 6214545
 GENERAL INFORMATION:
 APPLICANT: Dong, Fang
 APPLICANT: Lymichev, Victor I.
 APPLICANT: Prudent, James R.
 APPLICANT: Dahberg, James E.
 APPLICANT: Fors, Lance
 TITLE OF INVENTION: Polymorphism Analysis By Nucleic Acid
 NUMBER OF SEQUENCES: 38
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: MEDLEN & CARROLL, LLP
 STREET: 220 Montgomery Street, Suite 2200
 CITY: San Francisco
 STATE: CA
 COUNTRY: USA
 ZIP: 94104
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/851,588
 FILING DATE:
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Ingolia, Diane E.
 REGISTRATION NUMBER: 40,027
 REFERENCE/DOCKET NUMBER: FORS-02277
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 705-8410
 TELEFAX: (415) 397-8338
 INFORMATION FOR SEQ ID NO: 25:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 21 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 MOLECULE TYPE: other nucleic acid
 DESCRIPTION: /desc = "DNA"
 US-08-851-588-25

Query Match 87.5%; Score 21; DB 4; Length 21;
 Best Local Similarity 100.0%; Pred. No. 0.00099; Mismatches 0; Indels 0; Gaps 0;
 Matches 21; Conservative 0; MisMatch 0; Indel 0;

QY 1 gcagaaaaggcttacccatgg 21
 DB 1 GCAGAAAGCGCTAGCCATGG 21

RESULT 19
 US-09-677-218B-25
 ; Sequence 25; Application US/09677218B
 ; Patient No. 6355437
 ; GENERAL INFORMATION:
 ; APPLICANT: Lyamichev, Victor I.
 ; Brow, Mary Ann D.
 ; Fors, Lance

TITLE OF INVENTION: TARGET-DEPENDENT REACTIONS USING STRUCTURE-BRIDGING OLIGONUCLEOTIDES

NUMBER OF SEQUENCES: 68

CORRESPONDENCE ADDRESS:

ADDRESSEE: MEDLEN & CARROLL, LLP

STREET: 220 Montgomery Street, Suite 2200

CITY: San Francisco

STATE: CA

COUNTRY: USA

ZIP: 94104

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MC-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/677,218B

FILING DATE: 02-Oct-2000

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/034,205

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Macknight, Kamrin T.

REGISTRATION NUMBER: 38,230

REFERENCE/DOCKET NUMBER: FORS-03268

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 705-8410

TELEFAX: (415) 397-8338

INFORMATION FOR SEQ ID NO: 25:

SEQUENCE CHARACTERISTICS:

LENGTH: 21 base Pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: other nucleic acid

DESCRIPTION: /desc = "DNA"

SEQUENCE DESCRIPTION: SEQ ID NO: 25:

US-09-677-218B-25

RESULT 20

US-09-677-192-25

; Sequence 25; Application US/09677192

; Patient No. 6358691

; GENERAL INFORMATION:

; APPLICANT: Lyamichev, Victor I.

; APPLICANT: Brow, Mary Ann D.

; APPLICANT: Fors, Lance

; APPLICANT: Neri, Bruce P.

; TITLE OF INVENTION: TARGET-DEPENDENT REACTIONS USING STRUCTURE-BRIDGING

; TITLE OF INVENTION: OLIGONUCLEOTIDES

; FILE REFERENCE: FORS-04708

CURRENT APPLICATION NUMBER: US/09/677,192

CURRENT FILING DATE: 2000-10-02

PRIOR APPLICATION NUMBER: 09/034,205

PRIOR FILING DATE: 1998-03-03

NUMBER OF SEQ ID NOS: 68

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO: 25

LENGTH: 21

TYPE: DNA

ORGANISM: Artificial sequence

FEATURE: Artificial sequence

OTHER INFORMATION: Description of Artificial sequence: Synthetic

US-09-677-192-25

Query Match 87.5%; Score 21; DB 4; Length 21;
 Best Local Similarity 100.0%; Pred. No. 0.00099; Mismatches 0; Indels 0; Gaps 0;
 Matches 21; Conservative 0; MisMatches 0; Del 0; Insert 0; Job time: 5904 sec

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1	1

Query Match 87.5%; Score 21; DB 4; Length 21;
 Best Local Similarity 100.0%; Pred. No. 0.00099; Mismatches 0; Indels 0; Gaps 0;
 Matches 21; Conservative 0; MisMatches 0; Del 0; Insert 0; Job time: 5904 sec

Qy	Db
gcagaaggcgcttagcatgg 21	gcagaaggcgcttagcatgg 21
1	1

>Tue Aug 27 15:49:44 2002

us-10-037-990a-1.oli.rni

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Run on: August 26, 2002, 22:17:11 ; Search time 119.4 Seconds
 OM nucleic - nucleic search, using sw model

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GenCore version 4.5	C	28	24	100.0	57	1	US-08-356-287-36	Sequence 36, Appl
	C	29	24	100.0	57	5	PCT-US93-04863-36	Sequence 36, Appl
	C	30	24	100.0	64	1	US-08-429-181-31	Sequence 31, Appl
	C	31	24	100.0	64	1	US-08-164-388-31	Sequence 31, Appl
	C	32	23	95.8	23	1	US-08-356-287-25	Sequence 25, Appl
	C	33	23	95.8	23	5	PCT-US93-04863-25	Sequence 20, Appl
	C	34	23	95.8	29	1	US-08-240-547-20	Sequence 27, Appl
	C	35	22	91.7	22	1	US-08-356-287-27	Sequence 27, Appl
	C	36	22	91.7	22	5	PCT-US93-04863-27	Sequence 3, Appl
	C	37	21	87.5	27	2	US-08-78-928-3	Sequence 2, Appl
	C	38	21	87.5	28	2	US-08-738-928-2	Sequence 4, Appl
	C	39	21	87.5	28	3	US-08-928-4	Sequence 35, Appl
	C	40	21	87.5	28	3	US-08-474-70B-35	Sequence 35, Appl
	C	41	21	87.5	28	5	PCT-US95-05812-35	Sequence 35, Appl

Word size : 21

Total number of hits satisfying chosen parameters: 41

Minimum DB seq length: 0

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Post-processing: Listing first 65 summaries

Database : Issued Patents NA:*

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6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Length	DB ID	Description
1	24	100.0	24	1	US-08-240-547-18
2	24	100.0	24	1	US-08-449-050-16
3	24	100.0	24	1	US-08-332-616A-8
4	24	100.0	24	1	US-08-317-220-8
5	24	100.0	24	1	US-08-675-153-8
6	24	100.0	24	1	US-08-244-116B-51
7	24	100.0	24	2	US-08-738-928-5
8	24	100.0	24	2	US-08-841-254-2
9	24	100.0	24	2	US-08-881-571-8
10	24	100.0	24	4	US-08-282-054-8
11	24	100.0	26	1	US-08-438-639-51
12	24	100.0	26	2	US-08-256-568B-4
13	24	100.0	26	4	US-09-038-369B-4
14	24	100.0	27	1	PCT-US93-00928-1
15	24	100.0	28	3	US-08-474-700B-12
16	24	100.0	28	5	PCT-US95-05812-12
17	24	100.0	33	1	US-08-442-144A-127
18	24	100.0	33	1	US-07-813-338A-11
19	24	100.0	33	2	US-08-470-9124-61
20	24	100.0	33	3	US-08-441-971-127
21	24	100.0	33	4	US-08-221-653-127
22	24	100.0	33	4	US-08-442-144A-127
23	24	100.0	33	4	US-08-441-970-127
24	24	100.0	53	1	US-08-429-181-16
25	24	100.0	53	1	US-08-429-181-49
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Query Match Best Local Similarity 100.0%; Score 24; DB 1; Length 24; Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	cgcgaagcacccatcaaggcgt	24
Db	1	crcgcaanacccatcatcgaggct	24

ALIGNMENTS

RESULT 2
US-08-449-050-16
; Sequence 16, Application US/08449050
; Patent No. 5561058
; GENERAL INFORMATION:
APPLICANT: Gelfand, David
APPLICANT: Myers, Thomas
APPLICANT: Siguia, Christopher
TITLE OF INVENTION: Reagents and Methods for Coupled High Polymerase Chain Reaction
TITLE OF INVENTION: Temperature Reverse Transcription and Polymerase Chain Reaction
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hoffmann-La Roche Inc.
STREET: 340 Kingsland Street
CITY: Nutley
STATE: New Jersey
COUNTRY: U.S.A.
ZIP: 07110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/449,050
FILING DATE:
CLASSIFICATION: 435
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
MOLECULE TYPE: genomic DNA
US-08-449-050-16

Query Match 100.0%; Score 24; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 3.4e-06; Mismatches 0; Indels 0; Gaps 0;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ctgcgaagcaccatcaggagt 24
Db 1 CTCGCAAGCACCTATCAGGAGT 24

RESULT 3
US-08-332-616A-8
; Sequence 8, Application US/08332616A
; Patent No. 5620852
; GENERAL INFORMATION:
APPLICANT: LIN, LILY
APPLICANT: CIRINO, GEORGE
APPLICANT: ZHU, YU SHENG
TITLE OF INVENTION: NUCLEIC ACID PREPARATION METHODS
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: MEDLEN & CARROLL
STREET: 220 MONTGOMERY STREET, SUITE 2200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/317,220
FILING DATE:
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US/08/044,649
FILING DATE:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/0901,545
FILING DATE: 19-JUN-1992
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/614,921
FILING DATE: 14-NOV-1990
ATTORNEY/AGENT INFORMATION:
NAME: CARROLL, PETER G.
REGISTRATION NUMBER: 32,837
REFERENCE/DOCKET NUMBER: HRI-00542
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 397-8338
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-332-616A-8

Query Match 100.0%; Score 24; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 3.4e-06; Mismatches 0; Indels 0; Gaps 0;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ctgcgaagcaccatcaggagt 24
Patent No. 5654179
; GENERAL INFORMATION:
APPLICANT: LIN, LILY
TITLE OF INVENTION: NUCLEIC ACID PREPARATION METHODS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: PETER G. CARROLL
STREET: 220 Montgomery Street, Suite 2200
CITY: San Francisco
STATE: California
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/317,220
FILING DATE:
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US/08/044,649
FILING DATE:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/0901,545
FILING DATE: 19-JUN-1992
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/614,921
FILING DATE: 14-NOV-1990
ATTORNEY/AGENT INFORMATION:
NAME: CARROLL, PETER G.
REGISTRATION NUMBER: 32,837
REFERENCE/DOCKET NUMBER: HRI-00542
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 base pairs

TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 ; US-08-317-220-8

Query Match 100.0%; Score 24; DB 1; Length 24;
 Best Local Similarity 100.0%; Pred. No. 3.4e-06;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ctcccaaggaccctatcaggcagt 24
 Db 1 CTCCGAAGGACCCATCAGGCAGT 24

RESULT 5
 Sequence 8, Application US/08675153
 Patent No. 567724
 GENERAL INFORMATION:
 APPLICANT: Dubois, Dwight
 APPLICANT: Winkler, Matthew L.
 APPLICANT: Paslosie, Brittian L.
 TITLE OF INVENTION: RIBONUCLEASE RESISTANT VIRAL
 NUMBER OF INVENTION: RNA STANDARDS
 NUMBER OF SEQUENCES: 8
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Arnold, White & Durkee
 STREET: P.O. Box 4433
 CITY: Houston
 STATE: Texas
 COUNTRY: United States of America
 ZIP: 77210
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08675.153
 FILING DATE: Concurrently Herewith
 CLASSIFICATION: 530
 ATTORNEY/AGENT INFORMATION:
 NAME: Wilson, Mark B.
 REFERENCE/DOCKET NUMBER: 37,259
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (512) 418-3000
 TELEFAX: (512) 474-7577
 INFORMATION FOR SEQ ID NO: 8:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 24 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: other nucleic acid
 DESCRIPTION: /desc = "synthetic DNA
 DESCRIPTION: oligonucleotide"
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 ORIGINAL SOURCE:
 ORGANISM: Hepatitis-C virus
 US-08-244-116B-51

Query Match 100.0%; Score 24; DB 1; Length 24;
 Best Local Similarity 100.0%; Pred. No. 3.4e-06;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ctcccaaggaccctatcaggcagt 24
 Db 1 CTCCGAAGGACCCATCAGGCAGT 24

RESULT 7
 Sequence 5, Application US/08738928
 Patent No. 587442
 GENERAL INFORMATION:
 APPLICANT: Tsang, Sue Y.
 TITLE OF INVENTION: Oligonucleotide Primers for Amplifying
 TITLE OF INVENTION: HCV Nucleic Acid
 NUMBER OF SEQUENCES: 5
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Hoffmann-La Roche Inc.
 STREET: 340 Kingsland Street
 CITY: Nutley
 STATE: NJ
 COUNTRY: U.S.A.
 ZIP: 07110
 COMPUTER READABLE FORM:

RESULT 6
 Sequence 5, Application US/08244116B
 Patent No. 5763159
 GENERAL INFORMATION:

MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/738,928
 FILING DATE:
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: Parry, Douglas A.
 REFERENCE/DOCKET NUMBER: 35, 321
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (510) 814-2974
 TELEX/FAX: (510) 814-2977
 INFORMATION FOR SEQ ID NO: 5:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 24 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 US-08-738-928-5

Query Match 100.0%; score 24; DB 2; Length 24;
 Best Local Similarity 100.0%; Pred. No. 3.4e-06;
 Matches 24; Conservative 0; Mismatches 0;
 Indels 0; Gaps 0;
 Qy 1 ctgcgaagccatcaggagt 24
 Db 1 CTCGCAGCACCTATCAGGAGT 24

RESULT 8
 Sequence 8, Application US/08841252
 Patent No. 5919625

GENERAL INFORMATION:
 APPLICANT: DUBOIS, DWIGHT
 APPLICANT: WINKLER, MATTHEW
 APPLICANT: PASLOKE, BRITTAN L.
 TITLE OF INVENTION: RIBONUCLEASE RESISTANT VIRAL RNA
 TITLE OF INVENTION: STANDARDS
 NUMBER OF SEQUENCES: 8
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: ARNOLD WHITE & DURKEE
 STREET: P.O. BOX 4433
 CITY: HOUSTON
 STATE: Texas
 COUNTRY: USA
 ZIP: 77210

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/881,571
 FILING DATE: Concurrently Herewith
 CLASSIFICATION: 435

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/675,153
 FILING DATE: 03-JUL-1996

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 60/021,145
 FILING DATE: 03-JUL-1996

ATTORNEY/AGENT INFORMATION:
 NAME: Wilson, Mark B.
 REGISTRATION NUMBER: 37,259
 REFERENCE/DOCKET NUMBER: AMBI:033

TELECOMMUNICATION INFORMATION:
 TELEPHONE: 512/418-3000
 TELEX/FAX: 512/474-7577

INFORMATION FOR SEQ ID NO: 8:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 24 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-08-881-571-8

Query Match 100.0%; Score 24; DB 2; Length 24;
 Best Local Similarity 100.0%; Pred. No. 3.4e-06;
 Matches 24; Conservative 0; Mismatches 0;
 Indels 0; Gaps 0;
 Qy 1 ctgcgaagccatcaggagt 24
 Db 1 CTCGCAGCACCTATCAGGAGT 24

RESULT 10
 US-09-282-054-8
 Sequence 8, Application US/09282054
 ; Patent No. 6214982

GENERAL INFORMATION:
 APPLICANT: Pasliske, Brittan L.
 APPLICANT: Dubois, Dwight
 APPLICANT: Brown, David
 APPLICANT: Winkler, Matthew
 TITLE OF INVENTION: RIBONUCLEASE RESISTANT RNA PREPARATION
 TITLE OF INVENTION: AND UTILIZATION
 NUMBER OF SEQUENCES: 8
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Arnold, White & Durkee
 STREET: P.O. Box 4433
 CITY: Houston
 STATE: Texas
 COUNTRY: USA
 ZIP: 77210

COMPUTER READABLE FORM:
 COMPUTER: IBM PC compatible
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 MEDIUM TYPE: Floppy disk
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/282,054
 FILING DATE:
 APPLICATION NUMBER: US 08/675,153
 FILING DATE:
 CLASSIFICATION:
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US/08/881,571
 FILING DATE:
 APPLICATION NUMBER: US 08/675,153
 FILING DATE:
 FILING DATE: 03-JUL-1996
 REFERENCE/DOCKET NUMBER: AMBI:033
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 512/474-7577
 TELEFAX: 512/474-7577
 INFORMATION FOR SEQ ID NO: 8:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 24 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 60/021,145
 FILING DATE: 03-JUL-1996
 ATTORNEY/AGENT INFORMATION:
 NAME: Wilson, Mark B.
 REFERENCE/DOCKET NUMBER: 37,259
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US/08/881,571
 FILING DATE:
 FILING DATE:
 FILING DATE: 03-JUL-1996
 REFERENCE/DOCKET NUMBER: AMBI:033
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 512/474-7577
 TELEFAX: 512/474-7577
 INFORMATION FOR SEQ ID NO: 8:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 24 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 ; US-09-282-054-8

Query Match 100.0%; Score 24; DB 4; Length 24;
 Best Local Similarity 100.0%; Pred. No. 3.4e-06;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 12
 US-08-256-568B-4
 ; Sequence 4, Application US/08256568B
 ; Patent No. 5846704

GENERAL INFORMATION:
 APPLICANT: MAERTENS, GEERT; STUYVER, LIEVEN;
 APPLICANT: ROSSAU, RUDI; VAN HEUVERSWYN, HUGO
 TITLE OF INVENTION: PROCESS FOR TYPING OF HCV
 TITLE OF INVENTION: ISOLATES
 NUMBER OF SEQUENCES: 97
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: BERNMAN & MOSERLIAN
 STREET: 600 THIRD AVENUE
 CITY: NEW YORK
 STATE: NEW YORK
 COUNTRY: USA
 ZIP: 10016

COMPUTER READABLE FORM:
 COMPUTER: IBM PC compatible
 MEDIUM TYPE: Floppy disk
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: ASCII
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/256,568B
 FILING DATE: 18-JUL-1994
 CLASSIFICATION: 435
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: PCT/EP93/03325

CORRESPONDENCE ADDRESS:
 ADDRESSEE: Hoffmann-La Roche Inc.
 STREET: 340 Kingsland Street
 CITY: Nutley
 STATE: NJ
 COUNTRY: U.S.A.
 ZIP: 07110-1199
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/240,547
 FILING DATE:
 CLASSIFICATION: 435
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US/07/918,844
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Slas Ph.D., Stacey R.
 REGISTRATION NUMBER: 32,630
 REFERENCE/DOCKET NUMBER: 8586
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (510) 814-8863
 TELEFAX: (510) 814-2977
 INFORMATION FOR SEQ ID NO: 19:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 26 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 ; US-08-240-547-19

Query Match 100.0%; Score 24; DB 1; Length 26;
 Best Local Similarity 100.0%; Pred. No. 3.4e-06;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ctgcgaagccatcatacgcagt 24
 Db 3 CTGCAGAGCACCTATCAGGCAGT 26

ATTORNEY/AGENT INFORMATION:

NAME: POREMSKI, PRISCILLA E.

REGISTRATION NUMBER: 33,207

REFERENCE/DOCKET NUMBER: 5532.PC.01

TELECOMMUNICATION INFORMATION:

TELEPHONE: 708-937-6365

TELEFAX: 708-937-9556

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 27 base Pairs

TYPE: NUCLEIC ACID

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

PCT-US93-00928-1

Query Match 100.0%; Score 24; DB 5; Length 27;
Best Local Similarity 100.0%; Pred. No. 3.4e-06;
Matches 24; Conservative 0; Mismatches 0;
Indels 0; Gaps 0;Qy 1 ctgcgaagccatcatacgagt 24
Db 3 CTGCAGACCCATCAGGAGT 25

RESULT 15

US-08-474-700B-12

Sequence 12, Application US/08474700B

; Patent No. 6001990

GENERAL INFORMATION:
APPLICANT: Wards, Jack
APPLICANT: Wakita, Takaji
APPLICANT: Moradpour, Darius
TITLE OF INVENTION: ANTISENSE INHIBITION OF HEPATITIS C VIRUS
NUMBER OF SEQUENCES: 45

CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish & Richardson P.C.

STREET: 225 Franklin Street

CITY: Boston

STATE: Massachusetts

COUNTRY: U.S.A.

ZIP: 02110-2804

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

COMPUTER: IBM PS/2 Model 50Z or 55SX

OPERATING SYSTEM: MS-DOS (Version 5.0)

SOFTWARE: Wordperfect (Version 5.1)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US95/05812

FILING DATE:

CLASSIFICATION:

PRIORITY APPLICATION DATA:

APPLICATION NUMBER: 08/240,382

FILING DATE: 10 May 1994

ATTORNEY/AGENT INFORMATION:

NAME: Clark, Paul T.

REGISTRATION NUMBER: 30,162

REFERENCE/DOCKET NUMBER: 00786/221001

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 542-5070

TELEFAX: (617) 542-8906

TELEX: 200154

INFORMATION FOR SEQ ID NO: 12:

SEQUENCE CHARACTERISTICS:

LENGTH: 28

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 542-5070

TELEFAX: (617) 542-8906

TELEX: 200154

INFORMATION FOR SEQ ID NO: 12:

SEQUENCE CHARACTERISTICS:

LENGTH: 28

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

US-08-474-700B-12

Query Match 100.0%; Score 24; DB 5; Length 28;
Best Local Similarity 100.0%; Pred. No. 3.4e-06;
Matches 24; Conservative 0; Mismatches 0;
Indels 0; Gaps 0;Qy 1 ctgcgaagccatcatacgagt 24
Db 2 CTGCAGACCCATCAGGAGT 25

RESULT 17

US-08-438-639-51

Sequence 51, Application US/08438639

; Patent No. 5712383

GENERAL INFORMATION:
APPLICANT: Sheridan, Patrick
APPLICANT: Chang, Chu-An
APPLICANT: Running, Joyce
APPLICANT: Urduia, Michael S.

TITLE OF INVENTION: PROBES FOR IMMOBILIZING NUCLEIC ACID

TITLE OF INVENTION: PROBES ON POLYSTYRENE SURFACES

Query Match 100.0%; Score 24; DB 3; Length 28;

NUMBER OF SEQUENCES: 70
 CORRESPONDENCE ADDRESS:
 ADDRESSE: CHIRON CORPORATION - R440
 STREET: P.O. Box 8097
 CITY: Emeryville
 STATE: CA
 COUNTRY: USA
 ZIP: 94662-8097
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/438,639
 FILING DATE: 10-MAY-1995
 CLASSIFICATION: 435
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 07/813,338
 FILING DATE: 23-DEC-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: Goldman, Kenneth, M.
 REFERENCE/DOCKET NUMBER: 34,174
 REGISTRATION NUMBER: 0232.001
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (510) 601-2719
 TELEX: N/A
 INFORMATION FOR SEQ ID NO: 51:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 33 base pairs
 SEQUENCE FOR SEQ ID NO: 51:
 LENGTH: 33 base pairs
 SEQUENCE CHARACTERISTICS:
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 ; US-08-438-639-51
 Query Match 100.0%; Score 24; DB 1; length 33;
 Best Local Similarity 100.0%; Pred. No. 3.4e-06; Mismatches 0; Indels 0; Gaps 0;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 ctccaaaggaccatcgccgac 24
 Db 7 CTCCAAAGCACCTATCAGGCACT 30
 RESULT 19
 Query Match 100.0%; Score 24; DB 1; length 33;
 Best Local Similarity 100.0%; Pred. No. 3.4e-06; Mismatches 0; Indels 0; Gaps 0;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 ctccaaaggaccatcgccgac 24
 Db 7 CTCCAAAGCACCTATCAGGCACT 30
 RESULT 18
 Query Match 100.0%; Score 24; DB 1; length 33;
 Best Local Similarity 100.0%; Pred. No. 3.4e-06; Mismatches 0; Indels 0; Gaps 0;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 ctccaaaggaccatcgccgac 24
 Db 7 CTCCAAAGCACCTATCAGGCACT 30
 RESULT 18
 Sequence 51, Application US/07813,338A
 Patent No. 5747244
 GENERAL INFORMATION:
 APPLICANT: Sheridan, Patrick
 APPLICANT: Chang, Chu-An
 APPLICANT: Running, Joyce
 APPLICANT: Urdia, Michael S.
 TITLE OF INVENTION: PROCESS FOR IMMOBILIZING NUCLEIC ACID
 NUMBER OF SEQUENCES: 70
 CORRESPONDENCE ADDRESS:
 ADDRESSE: CHIRON CORPORATION - R440
 STREET: P.O. Box 8097
 CITY: Emeryville
 STATE: CA
 COUNTRY: USA
 ZIP: 94662-8097
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/470,124
 FILING DATE:
 CLASSIFICATION:
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: 07/813,588
 FILING DATE: 23 December 1991
 ATTORNEY/AGENT INFORMATION:
 NAME: Ciotti, Thomas E.
 REFERENCE/DOCKET NUMBER: 22300-20104.20
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415-813-6600
 TELEX: 706141
 INFORMATION FOR SEQ ID NO: 61:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 33 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 ; US-07-813-338A-51

US-08-470-124-61

Sequence 127, Application US/08221653

Patent No. 61,90864

GENERAL INFORMATION:

APPLICANT: Tai-An Cha

TITLE OF INVENTION: HCV GENOMIC SEQUENCES FOR

NUMBER OF SEQUENCES: 147

CORRESPONDENCE ADDRESS:

ADDRESSEE: Wolf, Greenfield & Sacks, P.C.

STREET: 600 Atlantic Avenue

CITY: Boston

STATE: Massachusetts

COUNTRY: USA

ZIP: 02210

COMPUTER READABLE FORM:

MEDIUM TYPE: Disquette, 5.25 inch

OPERATING SYSTEM: IBM compatible

SOFTWARE: Wordperfect 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/221,653

FILING DATE:

CLASSIFICATION: 435

PRIORITY APPLICATION DATA:

APPLICATION NUMBER: US/07/881,528

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Janiuk, Anthony J.

REGISTRATION NUMBER: 29,809

REFERENCE/DOCKET NUMBER: C0772/7000

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 720-3500

TELEFAX: (617) 720-2441

TELEX: EZEKIEL

INFORMATION FOR SEQ ID NO: 127:

SEQUENCE CHARACTERISTICS:

LENGTH: 33 nucleotides

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA

US-08-221-653-127

Query Match 100.0%; Score 24; DB 4; Length 33;

Best Local Similarity 100.0%; Pred. No. 3.4e-06; Mismatches 0; Indels 0; Gaps 0;

Matches 24; Conservative 100.0%; Mismatches 0; Indels 0; Gaps 0;

GENERAL INFORMATION:

APPLICANT: Tai-An Cha

APPLICANT: Eileen Beall

APPLICANT: Bruce Irvine

APPLICANT: Janice Kolberg

APPLICANT: Michael S. Urdrea

TITLE OF INVENTION: HCV GENOMIC SEQUENCES FOR

NUMBER OF SEQUENCES: 148

CORRESPONDENCE ADDRESS:

ADDRESSEE: Chiron Corporation

STREET: 4560 Horton Street

CITY: Emeryville

STATE: California

RESULT 20

US-08-441-971-127

Sequence 127, Application US/08221653

Query Match 100.0%; Score 24; DB 3; Length 33;

Best Local Similarity 100.0%; Pred. No. 3.4e-06; Mismatches 0; Indels 0; Gaps 0;

Matches 24; Conservative 100.0%; Mismatches 0; Indels 0; Gaps 0;

GENERAL INFORMATION:

APPLICANT: Tai-An Cha

APPLICANT: Eileen Beall

APPLICANT: Bruce Irvine

APPLICANT: Janice Kolberg

APPLICANT: Michael S. Urdrea

TITLE OF INVENTION: HCV GENOMIC SEQUENCES FOR

NUMBER OF SEQUENCES: 148

CORRESPONDENCE ADDRESS:

ADDRESSEE: Chiron Corporation

STREET: 4560 Horton Street

CITY: Emeryville

STATE: California

RESULT 21

US-08-221-653-127

COUNTRY: USA
 ZIP: 94608-2916
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette, 3.5 Inch
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: Windows NT
 SOFTWARE: Microsoft Word 97
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/442,14A
 FILING DATE: MAY 15, 1995
 CLASSIFICATION: 435
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: 08/221,653
 FILING DATE: APRIL 1, 1994
 ATTORNEY/AGENT INFORMATION:
 NAME: Doreen Yatko Trujillo
 REGISTRATION NUMBER: 35,719
 REFERENCE/DOCKET NUMBER: CHIR-0121
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 215-568-3100
 TELEX: 215-568-3439
 INFORMATION FOR SEQ ID NO: 127:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 33 Nucleotides
 STRANDEDNESS: Single
 TOPOLogy: Linear
 MOLECULE TYPE: DNA
 US-08-442-144A-127

RESULT 23
 US-08-441-970-127
 Sequence 127, Application US/08441970

PATENT NO. 629370
 GENERAL INFORMATION:
 APPLICANT: Tai-An Cha
 TITLE OF INVENTION: HCV GENOMIC SEQUENCES FOR
 TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
 NUMBER OF SEQUENCES: 147
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
 STREET: 600 Atlantic Avenue
 CITY: Boston
 STATE: Massachusetts
 COUNTRY: USA
 ZIP: 02210

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30B
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/429,181
 FILING DATE: 26-APR-1995
 CLASSIFICATION: 435
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 08/164,388
 FILING DATE: 08-DEC-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: GOLDMAN, KENNETH M.
 REGISTRATION NUMBER: 34,174
 REFERENCE/DOCKET NUMBER: 0300.001
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (510) 601-2719
 TELEX: (510) 655-3542
 INFORMATION FOR SEQ ID NO: 16:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 53 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLogy: Linear
 MOLECULE TYPE: DNA (genomic)
 US-08-429-181-16

REGISTRATION NUMBER: 29,809
 REFERENCE/DOCKET NUMBER: C0727/7000
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617) 720-3500
 TELEX: (617) 720-2441
 INFORMATION FOR SEQ ID NO: 127:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 33 nucleotides
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLogy: Linear
 MOLECULE TYPE: DNA
 US-08-441-970-127

Query Match 100 %; Score 24; DB 4; Length 33;
 Best Local Similarity 100 %; Pred. No. 3.4e-06; Mismatches 0;
 Matches 24; Conservative 0; Indels 0; Gaps 0;
 Qy 1 ctgcgaagccatcaggact 24
 Db 7 CTCGCAAGCACCTATCAGGCACT 30

RESULT 24
 US-08-429-181-16
 Sequence 16, Application US/08429181
 PATENT NO. 5035352
 GENERAL INFORMATION:
 APPLICANT: URDEA, MICHAEL S.
 APPLICANT: FULTZ, TIMOTHY
 APPLICANT: WARNER, BRIAN D.
 APPLICANT: COLLINS, MARK
 TITLE OF INVENTION: SOLUTION PHASE NUCLEIC ACID SANDWICH
 NUMBER OF SEQUENCES: 61
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: CHIRON CORPORATION - INTELLECTUAL PROPERTY
 ADDRESSEE: R440
 STREET: 4560 HORTON STREET
 CITY: EMERYVILLE
 STATE: CALIFORNIA
 COUNTRY: USA
 ZIP: 94608-2916

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30B
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/429,181
 FILING DATE: 26-APR-1995
 CLASSIFICATION: 435
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 08/164,388
 FILING DATE: 08-DEC-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: GOLDMAN, KENNETH M.
 REGISTRATION NUMBER: 34,174
 REFERENCE/DOCKET NUMBER: 0300.001
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (510) 601-2719
 TELEX: (510) 655-3542
 INFORMATION FOR SEQ ID NO: 16:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 53 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLogy: Linear
 MOLECULE TYPE: DNA (genomic)
 US-08-429-181-16

RESULT 25
 US-08-429-181-49
 ; Sequence 49, Application US/08429181
 ; Patent No. 633532
 ; GENERAL INFORMATION:
 ; APPLICANT: URBEA, MICHAEL S.
 ; APPLICANT: FULTZ, TIMOTHY
 ; APPLICANT: WARNER, BRIAN D.
 ; APPLICANT: COLLINS, MARK
 ; APPLICANT: WARNER, BRIAN D.
 ; APPLICANT: FULTZ, TIMOTHY
 ; APPLICANT: COLLINS, MARK
 ; TITLE OF INVENTION: SOLUTION PHASE NUCLEIC ACID SANDWICH
 ; TITLE OF INVENTION: ASSAYS HAVING REDUCED BACKGROUND NOISE
 ; NUMBER OF SEQUENCES: 61
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: CHIRON CORPORATION - INTELLECTUAL PROPERTY
 ; STREET: 4560 HORTON STREET
 ; CITY: EMERYVILLE
 ; STATE: CALIFORNIA
 ; COUNTRY: USA
 ; ZIP: 94608-2916
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent Release #1.0, Version #1.30B
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08429,181
 ; FILING DATE: 26 APR-1995
 ; CLASSIFICATION: 435
 ; PRIORITY APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/164,388
 ; FILING DATE: 08-DEC-1993
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: GOLDMAN, KENNETH M.
 ; REGISTRATION NUMBER: 34,174
 ; REFERENCE/DOCKET NUMBER: 0300.001
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (510) 601-2719
 ; TELEFAX: (510) 655-3542
 ; TELEX: N/A
 ; INFORMATION FOR SEQ ID NO: 16:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 53 base Pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: DNA (genomic)
 ; US-08-164-388-16
 ;
 RESULT 27
 Query Match 100 0%; Score 24; DB 1; Length 53;
 Best Local Similarity 100 0%; Pred. No. 3.4e-06; Mismatches 0; Indels 0; Gaps 0;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 ctgcgaagcccttcaggcgt 24
 Oy 1 ctgcgaagcccttcaggcgt 24
 Db 27 CTGCAGACCTATCAGGCACT 50
 ;
 RESULT 26
 US-08-164-388-16
 ; Sequence 16, Application US/08164388

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30B
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/164, 388
 FILING DATE: 08-DEC-1993
 CLASSIFICATION: 436
 ATTORNEY/AGENT INFORMATION:
 NAME: GOLDMAN, KENNETH M.
 REGISTRATION NUMBER: 34,174
 REFERENCE/DOCKET NUMBER: 0300.001
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (510) 601-2719
 TELEX: N/A
 INFORMATION FOR SEQ ID NO: 49:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 53 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 US-08-164-388-49

RESULT 28

Query Match 100.0%; Score 24; DB 1; Length 53;
 Best Local Similarity 100.0%; Pred. No. 3.4e-06;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ctccaaaggaccctatcaggagt 24
 Db 27 CTCCAAAGCACCTATCAGGAGT 50

US-08-356-287-36/c

Sequence 36 Application US/08356287
 Patent No. 5686272
 GENERAL INFORMATION:
 APPLICANT: Ronald L. Marshall
 APPLICANT: John J. Carrino
 APPLICANT: Joann Sustachek
 TITLE OF INVENTION: AMPLIFICATION OF RNA SEQUENCES USING THE LIGASE CHAIN REACTION
 NUMBER OF SEQUENCES: 36

RESULT 29

Query Match 100.0%; Score 24; DB 1; Length 57;
 Best Local Similarity 100.0%; Pred. No. 3.4e-06;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ctcgaaaggccctatcaggagt 24
 Db 57 CTCGAAAGCACCTATCAGGAGT 34

PCT-US93-04863-36/c

Sequence 36 Application PC/TUS9304863
 GENERAL INFORMATION:
 APPLICANT: Ronald L. Marshall
 APPLICANT: John J. Carrino
 APPLICANT: Joann C. Sustachek
 ADDRESS: Abbott Laboratories
 STREET: One Abbott Park Road
 CITY: Abbott Park
 STATE: Illinois
 COUNTRY: USA
 ZIP: 60064-3500

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy diskette
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Wordperfect
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/US93/04863
 FILING DATE: 19930524
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/891,543
 FILING DATE: 29 MAY 1992
 ATTORNEY/AGENT INFORMATION:
 NAME: Thomas D. Baird
 REGISTRATION NUMBER: 32,459
 REFERENCE/DOCKET NUMBER: 5172.PC.01
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 708-937-4804
 TELEX: 708-938-2623
 INFORMATION FOR SEQ ID NO: 36:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 57
 TYPE: NUCLEIC ACID
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: RNA
 PCT-US93-04863-36

Query Match 100.0%; Score 24; DB 5; Length 57;
 Best Local Similarity 100.0%; Pred. No. 3.4e-06;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ctcgaaaggccctatcaggagt 24
 Db 57 CTCGAAAGCACCTATCAGGAGT 34

US-08-356-287-36

RESULT 30
 US-08-429-181-31
 ; Sequence 31, Application US/08429181
 ; Patent No. 5635352
 GENERAL INFORMATION:
 APPLICANT: URDEA, MICHAEL S.
 APPLICANT: FULTZ, TIMOTHY
 APPLICANT: WARNER, BRIAN D.
 APPLICANT: COLLINS, MARK
 TITLE OF INVENTION: SOLUTION PHASE NUCLEIC ACID SANDWICH
 TITLE OF INVENTION: ASSAYS HAVING REDUCED BACKGROUND NOISE
 NUMBER OF SEQUENCES: 61
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: CHIRON CORPORATION - INTELLECTUAL PROPERTY
 ADDRESS: R44
 STREET: 4560 HORTON STREET
 CITY: EMERYVILLE
 STATE: CALIFORNIA
 ZIP: 94608-2916
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, version #11.30B
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08429, 181
 FILING DATE: 26-APR-1995
 CLASSIFICATION: 435
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 08/164, 388
 FILING DATE: 08-DEC-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: GOLDMAN, KENNETH M.
 REGISTRATION NUMBER: 34,174
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (510) 601-2719
 TELEFAX: (510) 655-3542
 INFORMATION FOR SEQ ID NO: 31:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 64 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 US-08-164-388-31

SEQUENCE CHARACTERISTICS:
 LENGTH: 64 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 INFORMATION FOR SEQ ID NO: 31:
 LENGTH: 64 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 US-08-429-181-31

Query Match 100.0%; Score 24; DB 1; Length 64;
 Best Local Similarity 100.0%; Pred. No. 3.4e-06;
 Matches 24; Conservative 0; Mismatches 0; Indels 0;
 Gaps 0;

Qy 1 ctgcgaaggccatcatacgact 24
 Db 23 CTCGCAGACCCCTATCAGGGT 46

RESULT 32
 US-08-356-287-25
 ; Sequence 25, Application US/08356287
 ; Patent No. 5666272
 GENERAL INFORMATION:
 APPLICANT: Ronald L. Marshall
 APPLICANT: John J. Carrino
 APPLICANT: Joann Sustacki
 TITLE OF INVENTION: AMPLIFICATION OF RNA SEQUENCES USING
 TITLE OF INVENTION: THE LIGASE CHAIN REACTION
 NUMBER OF SEQUENCES: 36
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Abbott Laboratories
 STREET: 100 Abbott Park Road
 CITY: Abbott Park
 STATE: Illinois
 COUNTRY: USA
 ZIP: 60064-3500
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy diskette
 COMPUTER: Macintosh
 OPERATING SYSTEM: System 7.0.1
 SOFTWARE: Microsoft Word 5.1a
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/356, 287
 FILING DATE:
 CLASSIFICATION: 435
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 07/891, 543

FILING DATE: 29 MAY 1992
 ATTORNEY/AGENT INFORMATION:
 NAME: Paul D. Yasger
 REGISTRATION NUMBER: 37,477
 REFERENCE/DOCKET NUMBER: 5172.US.P1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 708-937-2341
 TELEFAX: 708-938-2623
 INFORMATION FOR SEQ ID NO: 25:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 23
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLogy: linear
 MOLECULE TYPE: Other nucleic acid (synthetic DNA)
 US-08-356-287-25

Query Match 95.8%; Score 23; DB 5; length 23;
 Best Local Similarity 100.0%; Pred No. 1.4e-05;
 Matches 23; Conservative 0; Mismatches 0;
 Indels 0; Gaps 0;

Qy 2 tcgcagcacccatcaggagt 24
 Db 1 TCGCAGCACCTATCAGGAGT 23

RESULT 34
 US-08-240-547-20
 Sequence 20, Application US/08240547
 Patent No. 5527660
 GENERAL INFORMATION:
 APPLICANT: Resnick, Robert M.
 TITLE OF INVENTION: Primers and Probes for Detection of Hepatitis C and No. 5527669el Variants
 NUMBER OF SEQUENCES: 43
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Hoffmann-La Roche Inc.
 STREET: 340 Kingsland Street
 CITY: Nutley
 STATE: NJ
 COUNTRY: U.S.A.
 ZIP: 07110-1199

COMPUTER READABLE FORM:
 COMPUTER: IBM PC compatible
 MEDIUM TYPE: Floppy disk
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, version #1.25

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/240,547
 FILING DATE: 29 MAY 1992
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/07/918,844
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Sias Ph.D., Stacey R.
 REGISTRATION NUMBER: 32,630
 REFERENCE/DOCKET NUMBER: 8586
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (510) 814-2863
 TELEFAX: (510) 814-2977
 INFORMATION FOR SEQ ID NO: 20:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 29 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLogy: linear
 MOLECULE TYPE: DNA (genomic)
 US-08-240-547-20

Query Match 95.8%; Score 23; DB 5; length 29;
 Best Local Similarity 100.0%; Pred No. 1.4e-05;
 Matches 23; Conservative 0; Mismatches 0;
 Indels 0; Gaps 0;

Qy 2 tcgcagcacccatcaggagt 24
 Db 7 TCGCAGCACCTATCAGGAGT 29

RESULT 35
 US-08-356-287-27/c
 Sequence 27, Application US/08356287
 Patent No. 5686272
 GENERAL INFORMATION:
 APPLICANT: Ronald L. Marshall
 APPLICANT: John J. Carrino
 APPLICANT: Joann C. Sustachek
 PCT-US93-04863-25

SEQUENCE CHARACTERISTICS:
 LENGTH: 23
 TYPE: NUCLEIC ACID
 STRANDEDNESS: Single
 TOPOLogy: Linear
 MOLECULE TYPE: Other nucleic acid (synthetic DNA)

TITLE OF INVENTION: AMPLIFICATION OF RNA SEQUENCES USING THE LIGASE CHAIN REACTION
 TITLE OF INVENTION: THE LIGASE CHAIN REACTION
 NUMBER OF SEQUENCES: 36
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Abbott Laboratories
 STREET: 100 Abbott Park Road
 CITY: Abbott Park
 STATE: Illinois
 COUNTRY: USA
 ZIP: 60064-3500
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy diskette
 COMPUTER: Macintosh
 OPERATING SYSTEM: System 7.0.1
 SOFTWARE: Microsoft Word 5.1a
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/356,287
 FILING DATE:
 CLASSIFICATION: 435
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 07/891,543
 FILING DATE: 29 MAY 1992
 ATTORNEY/AGENT INFORMATION:
 NAME: Paul D. Yasger
 REGISTRATION NUMBER: 37,477
 REFERENCE/DOCKET NUMBER: 5172.US.P1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 708-937-2341
 TELEFAX: 708-938-2623
 INFORMATION FOR SEQ ID NO: 27:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 22
 TYPE: nucleic acid
 STRANDEDNESS: single
 MOLECULE TYPE: Other nucleic acid (synthetic DNA)
 US-08-356-287-27

RESULT 36
 PCT-US93-04863-27/C
 Sequence 27, Application PC/TUS9304863
 GENERAL INFORMATION:
 APPLICANT: Ronald L. Marshall
 APPLICANT: John J. Carrino
 APPLICANT: John C. Sustachek
 APPLICANT: Abbott Laboratories
 TITLE OF INVENTION: AMPLIFICATION OF RNA SEQUENCES
 TITLE OF INVENTION: USING THE LIGASE CHAIN REACTION
 NUMBER OF SEQUENCES: 36
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Abbott Laboratories
 STREET: One Abbott Park Road
 CITY: Abbott Park
 STATE: Illinois
 COUNTRY: USA
 ZIP: 60064-3500
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy diskette
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/738,928
 FILING DATE:
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: PETRY, Douglas A.
 REGISTRATION NUMBER: 35,321
 REFERENCE/DOCKET NUMBER: 9263
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (510) 814-2974
 TELEFAX: (510) 814-2977
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 27 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 US-08-738-928-3

Query Match 87.5%; Score 21; DB 2; Length 27;
Best Local Similarity 100.0%; Pred. No. 0.00023; Mismatches 0; Indels 0; Gaps 0;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 gcaagcacctatcaggcgt 24
Db 1 |||||GCAGCACCTATCAGGCGT 21

RESULT 38
US-08-738-928-2
; Sequence 2, Application US/08738928
; Patent No. 5837442
; GENERAL INFORMATION:
; APPLICANT: Tsang, Sue Y.
; TITLE OF INVENTION: Oligonucleotide Primers for Amplifying
; TITLE OF INVENTION: HCV Nucleic Acid
; NUMBER OF SEQUENCES: 5
; CURRENT APPLICATION ADDRESS:
; ADDRESSEE: Hoffmann-La Roche Inc.
; STREET: 340 Kingsland Street
; CITY: Nutley
; STATE: NJ
; ZIP: 07110
; COMPUTER READABLE FORM:
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patientin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/738,928
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Petry, Douglas A.
; REGISTRATION NUMBER: 35,321
; REFERENCE/DOCKET NUMBER: 9263
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 814-2974
; TELEFAX: (510) 814-2977
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-738-928-2

Query Match 87.5%; Score 21; DB 3; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.00023; Mismatches 0; Indels 0; Gaps 0;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 gcaagcacctatcaggcgt 24
Db 1 |||||GCAGCACCTATCAGGCGT 21

RESULT 40
US-08-474-700B-35/C
; Sequence 35, Application US/08474700B
; Patent No. 6001990
; GENERAL INFORMATION:
; APPLICANT: Wands, Jack
; APPLICANT: Wakita, Takaji
; APPLICANT: Motradpour, Darius
; TITLE OF INVENTION: ANTISENSE INHIBITION OF HEPATITIS C
; TITLE OF INVENTION: VIRUS
; NUMBER OF SEQUENCES: 45
; CURRENT APPLICATION ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; COMPUTER: IBM PS/2 Model 50Z or 55SX
; OPERATING SYSTEM: MS-DOS (Version 5.0)
; SOFTWARE: Wordperfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/474,700B
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/240,382
; FILING DATE: 10 May 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Fraser, Janis K.
; REGISTRATION NUMBER: 34,819
; REFERENCE/DOCKET NUMBER: 00786/279001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 35:

Query Match 87.5%; Score 21; DB 2; Length 27;
Best Local Similarity 100.0%; Pred. No. 0.00023; Mismatches 0; Indels 0; Gaps 0;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 gcaagcacctatcaggcgt 24
Db 1 |||||GCAGCACCTATCAGGCGT 21

RESULT 39
US-09-039-866-4
; Sequence 4, Application US/09039866
; Patent No. 6001611
; GENERAL INFORMATION:
; APPLICANT: Will, Stephen G.
; TITLE OF INVENTION: MODIFIED NUCLEIC ACID AMPLIFICATION
; TITLE OF INVENTION: PRIMERS
; NUMBER OF SEQUENCES: 7
; CURRENT APPLICATION ADDRESS:
; ADDRESSEE: Roche Molecular Systems
; STREET: 1080 U.S. Highway 202
; CITY: Branchburg

Job time: 5905 sec

SEQUENCE CHARACTERISTICS:
 LENGTH: 28
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-08-474-700B-35

Query Match 87.5%; Score 21; DB 3; Length 28;
 Best Local Similarity 100.0%; Pred. No. 0.00023; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ctgcgaaacgaccatcaggc 21
 Db 21 CTCGCAAGCACCCATCAGGC 1

RESULT 41

PCT-US95-05812-35/c

Sequence 35, Application PC/TUS9505812

GENERAL INFORMATION:

APPLICANT: Wakita, Takaji

TITLE OF INVENTION: ANTISENSE INHIBITION OF

TITLE OF INVENTION: HEPATITIS C VIRUS

NUMBER OF SEQUENCES: 38

CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish & Richardson

STREET: 225 Franklin Street

CITY: Boston

STATE: Massachusetts

COUNTRY: U.S.A.

ZIP: 02110-2804

COMPUTER READABLE FORM:

MEDIUM TYPE: 3 1/2" DISKETTE, 1.44 MB

COMPUTER: IBM PS/2 Model 50Z or 55SX

OPERATING SYSTEM: MS-DOS (Version 5.0)

SOFTWARE: Wordperfect (Version 5.1)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US95/05812

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/740,382

FILING DATE: 10 May 1994

ATTORNEY/AGENT INFORMATION:

NAME: Clark, Paul T.

REGISTRATION NUMBER: 30,162

REFERENCE/DOCKET NUMBER: 00786/221001

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 542-5070

TELEFAX: (617) 542-8906

TELEX: 200154

INFORMATION FOR SEQ ID NO: 35:

SEQUENCE CHARACTERISTICS:

LENGTH: 28

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

PCT-US95-05812-35

Query Match 87.5%; Score 21; DB 5; Length 28;
 Best Local Similarity 100.0%; Pred. No. 0.00023; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ctgcgaaacgaccatcaggc 21
 Db 21 CTCGCAAGCACCCATCAGGC 1

Tue Aug 27 15:49:50 2002

us-10-037-990a-2.oli.rni

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: August 26, 2002, 22:14:58 ; Search time 3233.25 Seconds
(without alignments)
100.186 Million cell updates/sec

Title: US-10-037-990a-2
Perfect score: 24
Sequence: 1 ctcgcgaagcacctatccaggagt 24

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 13736207 seqs, 6748477542 residues
Word size : 21

Total number of hits satisfying chosen parameters: 0
Minimum DB seq length: 0
Maximum DB seq length: 100

Post-processing: Listing first 65 summaries

Database :	EST:*
1:	em_estba:*
2:	em_estchum:*
3:	em_estin:*
4:	em_estmu:*
5:	em_estov:*
6:	em_estpl:*
7:	em_estro:*
8:	em_htc:*
9:	gb_est1:*
10:	gb_est2:*
11:	gb_htc:*
12:	gb_gss:*
13:	em_gss_hun:*
14:	em_gss_inv:*
15:	em_gss_pbn:*
16:	em_gss_vrt:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
..

No matches found

Search completed: August 26, 2002, 22:14:58
Job time: 9022 sec

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GenCore version 4.5
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OM nucleic - nucleic search, using sw model
Run on: August 26, 2002, 21:20:52 ; Search time 1915.63 Seconds
(without alignments)
262.178 Million cell updates/sec

Title: US-10-037-990a-2
Perfect score: 24
Sequence: 1 ctccgaaagcacctatcaggcgt 24

Scoring table: Oligo-NIC
Gapop 60.0 , Gapext 60.0

Searched: 1797656 seqs, 10463268293 residues

Word size : 21

Total number of hits satisfying chosen parameters: 54
Minimum DB seq length: 0
Maximum DB seq length: 100

Post-processing: Listing first 65 summaries
Database : GenEmbl:
1: gb_ba:*

2: gb_hhg:*

3: gb_in:*

4: gb_on:*

5: gb_ov:*

6: gb_pat:*

7: gb_ph:*

8: gb_pl:*

9: gb_ppl:*

10: gb_ro:*

11: gb_sts:*

12: gb_sy:*

13: gb_un:*

14: gb_vl:*

15: em_ba:*

16: em_fun:*

17: em_hum:*

18: em_in:*

19: em_mu:*

20: em_on:*

21: em_or:*

22: em_ov:*

23: em_Pat:*

24: em_ph:*

25: em_pl:*

26: em_ro:*

27: em_sts:*

28: em_un:*

29: em_vl:*

30: em_htg_hum:*

31: em_htg_inv:*

32: em_htg_other:*

33: em_htgo_inv:*

SUMMARIES

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

ALIGNMENTS

RESULT	1	RESULT	1	RESULT	1	RESULT	1
LOCUS	A68286	DEFINITION	Sequence 7 from Patent WO9716716.	DNA	linear	PAT	06-MAY-1999
ACCESSION	A68286						
VERSION	A68286.1	TITLE	GI:4759407				
KEYWORDS							
SOURCE							
ORGANISM	unclassified						

REFERENCE
1 (bases 1 to 24)

AUTHORS
Bosio, P., Strunica, C. and Clementza, F.

TITLE
METHOD TO DETECT HOW SPECIFIC NUCLEIC ACIDS

JOURNAL
Patent: WO 9716716-A 7 NOV-1997;

COMMENT	WABCO B.V. (NL)
FEATURES	Other publication IT RM960404 19971209.
source	Location/Qualifiers
	1. .24 /organism="unidentified" /db_xref="taxon:32644"
BASE COUNT	6 a 9 c 5 g 4 t
ORIGIN	
RESULT	2
Qy	1 ctgcgaagcacccatcagcagt 24
LOCUS	AX003942
DEFINITION	Sequence 2 from Patent WO9923249.
ACCESSION	AX003942
VERSION	AX003942.1 GT:9927502
KEYWORDS	synthetic construct.
SOURCE	synthetic construct.
REFERENCE	artificial sequence.
AUTHORS	Kessler,C. and Bartl,K.
TITLE	Specific and sensitive method for detecting nucleic acids
JOURNAL	Patent: WO 9923249-A 2 14-MAY-1999;
FEATURES	KESSLER CHRISTOPH (DE); BARTL KURT (DE)
source	Location/Qualifiers
ORGANISM	1. .24 /organism="synthetic construct" /db_xref="taxon:32630" /note="K778"
REFERENCE	1. (bases 1 to 24)
AUTHORS	Simmonds,P., Chan,S.-W. and Yap,P.Lee.
TITLE	Hepatitis-C virus testing
JOURNAL	Patent: US 5763159-A 51 09-JUN-1998;
FEATURES	Location/Qualifiers
source	1. .24 /organism="unknown"
BASE COUNT	4 a 5 c 9 g 6 t
ORIGIN	
Query Match	100.0%; Score 24; DB 6; Length 24;
Best Local Similarity	100.0%; Pred. No. 0.00034; Mismatches 0;
Matches	Indels 0; Gaps 0;
Qy	1 ctgcgaagcacccatcagcagt 24
LOCUS	AR011642
DEFINITION	Sequence 51 from patent US 5763159.
ACCESSION	AR011642
VERSION	AR011642.1 GT:3969632
KEYWORDS	Unknown.
SOURCE	Unclassified.
ORGANISM	
REFERENCE	1. (bases 1 to 24)
AUTHORS	Simmonds,P., Chan,S.-W. and Yap,P.Lee.
TITLE	Hepatitis-C virus testing
JOURNAL	Patent: US 5763159-A 51 09-JUN-1998;
FEATURES	Location/Qualifiers
source	1. .24 /organism="unknown"
BASE COUNT	4 a 5 c 9 g 6 t
ORIGIN	
Query Match	100.0%; Score 24; DB 6; Length 24;
Best Local Similarity	100.0%; Pred. No. 0.00034; Mismatches 0;
Matches	Indels 0; Gaps 0;
Qy	1 ctgcgaagcacccatcagcagt 24
LOCUS	AR011642
DEFINITION	Sequence 51 from patent US 5763159.
ACCESSION	AR011642
VERSION	AR011642.1 GT:3969632
KEYWORDS	Unknown.
SOURCE	Unclassified.
ORGANISM	
REFERENCE	1. (bases 1 to 24)
AUTHORS	Simmonds,P., Chan,S.-W. and Yap,P.Lee.
TITLE	Hepatitis-C virus testing
JOURNAL	Patent: US 5763159-A 51 09-JUN-1998;
FEATURES	Location/Qualifiers
source	1. .24 /organism="unknown"
BASE COUNT	4 a 5 c 9 g 6 t
ORIGIN	
Query Match	100.0%; Score 24; DB 6; Length 24;
Best Local Similarity	100.0%; Pred. No. 0.00034; Mismatches 0;
Matches	Indels 0; Gaps 0;
Qy	1 ctgcgaagcacccatcagcagt 24
LOCUS	AR021564
DEFINITION	Sequence 2 from Patent WO9924606.
ACCESSION	AX021564
VERSION	AX021564.1 GT:10044848
KEYWORDS	
SOURCE	Hepatitis C virus.
ORGANISM	Hepatitis C virus.
REFERENCE	Viruses; ssRNA positive-strand viruses, no DNA stage: Flaviviridae; Hepacivirus.
AUTHORS	1. (bases 1 to 24)
TITLE	Kessler,C., Bartl,K., Haberhausen,G. and Orum,H.
JOURNAL	Specific and sensitive nucleic acid detection method
FEATURES	Patent: WO 9924606-A 2 20-MAY-1999;
source	KESSLER CHRISTOPH (DE); BARTL KURT (DE); HABERHAUSEN GERD (DE); ROCHE DIAGNOSTICS GMBH (DE); ORUM HENRIK (DK)
ORGANISM	Location/Qualifiers
REFERENCE	1. (bases 1 to 24)
AUTHORS	Tsang,S.Yen.
TITLE	Oligonucleotide primers for amplifying HCV nucleic acid
JOURNAL	Patent: US 5837424-A 17-Nov-1998;
FEATURES	Location/Qualifiers
source	1. .24 /organism="Hepatitis C virus", /db_xref="taxon:11103", /note="HCV primers"
BASE COUNT	6 a 9 c 5 g 4 t
ORIGIN	
Query Match	100.0%; Score 24; DB 6; Length 24;
Best Local Similarity	100.0%; Pred. No. 0.00034; Mismatches 0;
Matches	Indels 0; Gaps 0;
Qy	1 ctgcgaagcacccatcagcagt 24
LOCUS	CTCGCAGCACCTATCAGGCAGT 24
DEFINITION	
ACCESSION	
VERSION	
KEYWORDS	
SOURCE	
REFERENCE	
AUTHORS	
TITLE	
JOURNAL	
FEATURES	
source	
ORGANISM	
REFERENCE	
AUTHORS	
TITLE	
JOURNAL	
FEATURES	
source	
BASE COUNT	6 a 9 c 5 g 4 t
ORIGIN	
Query Match	100.0%; Score 24; DB 6; Length 24;
Best Local Similarity	100.0%; Pred. No. 0.00034; Mismatches 0;
Matches	Indels 0; Gaps 0;
Qy	1 ctgcgaagcacccatcagcagt 24
LOCUS	CTCGCAGCACCTATCAGGCAGT 24
DEFINITION	
ACCESSION	
VERSION	
KEYWORDS	
SOURCE	
REFERENCE	
AUTHORS	
TITLE	
JOURNAL	
FEATURES	
source	
ORGANISM	

RESULT 6
 AX021623 LOCUS AX021623 Sequence 2 from Patent WO9923250. DNA linear PAT 07-SEP-2000
 DEFINITION Sequence 2 from Patent WO9923250.
 ACCESSION AX021623
 KEYWORDS Hepatitis C virus.
 SOURCE Hepatitis C viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae; Hepacivirus.
 FEATURES source
 AUTHORS Kessler,C., Bartl,K., Haberhausen,G. and Orum,H.
 TITLE Specific and sensitive method for detecting nucleic acids
 JOURNAL Patent: WO 99/3250-A2 14-MAY-1999;
 KESSLER CHRISTOPH (DE); BARTL, KNOT (DE); HABERHAUSEN GERD (DE); ROCHE DIAGNOSTICS GMBH (DE); ORUM HENRIK (DK)
 Location/Qualifiers
 BASE COUNT 6 a 9 c 5 g 4 t
 ORIGIN /db_xref="taxon:11103"
 /organism="Hepatitis C virus"
 /db_xref="taxon:11103"
 /note="Synthetic oligonucleotide primer (HCV reverse)"
 RESULT 7
 AX040437 LOCUS AX040437 Sequence 2 from Patent WO0063444. DNA linear PAT 18-NOV-2000
 DEFINITION Sequence 2 from Patent WO0063444.
 ACCESSION AX040437
 VERSION 1.1
 KEYWORDS Hepatitis C virus.
 SOURCE Hepatitis C viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae; Hepacivirus.
 REFERENCES 1 (bases 1 to 24)
 AUTHORS Budzka,A., Maillard,P., Nitkiewicz,J. and Crainic,R.
 TITLE Method for detecting hepatitis C virus with hybridomas
 JOURNAL Patent: WO 00/63444-A2 26-OCT-2000;
 INSTITUT PASTEUR (FR)
 FEATURES source
 BASE COUNT 6 a 9 c 5 g 4 t
 ORIGIN /organism="Hepatitis C virus"
 /db_xref="taxon:11103"
 /note="Bases 1 to 24"
 /organism="Hepatitis C virus"
 /db_xref="taxon:11103"
 /note="Bases 1 to 24"
 RESULT 8
 AX147012 LOCUS AX147012 Sequence 6 from Patent WO0137291. DNA linear PAT 08-JUN-2001
 DEFINITION Sequence 6 from Patent WO0137291.
 ACCESSION AX147012
 VERSION AX147012.1
 KEYWORDS Hepatitis C virus.
 SOURCE Hepatitis C viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae; Hepacivirus.
 FEATURES source
 AUTHORS Kessler,C., Bartl,K., Haberhausen,G. and Orum,H.
 TITLE Specific and sensitive method for detecting nucleic acids
 JOURNAL Patent: WO 01/37291-A 6 25-MAY-2001;
 Roche Diagnostics GmbH (DE)
 Location/Qualifiers
 BASE COUNT 6 a 9 c 5 g 4 t
 ORIGIN /organism="synthetic construct"
 /db_xref="taxon:32650"
 /note="Synthetic oligonucleotide primer (HCV reverse)"
 /note="Biotin derivatization"
 RESULT 9
 I22159 LOCUS I22159 Sequence 18 from patent US 5527669. DNA linear PAT 07-OCT-1996
 DEFINITION Sequence 18 from patent US 5527669.
 ACCESSION I22159
 VERSION 1.1
 KEYWORDS Unknown.
 SOURCE Unknown.
 REFERENCES 1 (bases 1 to 24)
 AUTHORS Resnick,R.M. and Young,K.K.Y.
 TITLE Methods, primers and probes for detection of hepatitis C and novel variants
 JOURNAL Patent: US 5527669-A 18-18-JUN-1996;
 FEATURES source
 BASE COUNT 6 a 9 c 5 g 4 t
 ORIGIN /organism="unknown"
 /note="Bases 1 to 24"
 /note="Bases 1 to 24"
 RESULT 10
 I26948 LOCUS I26948 Sequence 16 from patent US 5561058. DNA linear PAT 07-OCT-1996
 DEFINITION Sequence 16 from patent US 5561058.
 ACCESSION I26948
 VERSION 1.1
 KEYWORDS Unknown.
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCES 1 (bases 1 to 24)
 AUTHORS Gelfand,D.H., Myers,T.W. and Siguia,C.L.

	TITLE	Methods for coupled high temperatures reverse transcription and polymerase chain reactions					
	JOURNAL	Patent: US 561058-A 16 01-OCT-1996;					
	FEATURES	Location/Qualifiers					
	source	1. .24 /organism="unknown"					
BASE COUNT	6 a	9 c	5 g	4 t			
ORIGIN							
RESULT	11						
140300	I40300	Sequence 8 from patent US 5620852.	24 bp	DNA	linear	PAT 13-MAY-1997	
LOCUS							
DEFINITION							
ACCESSION	I40300						
VERSION	140300.1						
KEYWORDS							
SOURCE							
ORGANISM	Unknown.						
REFERENCE							
AUTHORS	Lin,L., Cimino,G. and Zhu,Y.S.						
TITLE	Nucleic acid preparation methods						
JOURNAL	Patent: US 5620852-A 8 15-APR-1997;						
FEATURES	1. .24 /organism="unknown"						
source							
BASE COUNT	6 a	9 c	5 g	4 t			
ORIGIN							
RESULT	13						
168635	I68635	Sequence 8 from patent US 5677124.	24 bp	DNA	linear	PAT 04-FEB-1998	
LOCUS							
DEFINITION							
ACCESSION	I68635						
VERSION	168635.1						
KEYWORDS							
SOURCE	Unknown.						
ORGANISM	Unclassified.						
REFERENCE							
AUTHORS	Dubois,D.B., Winkler,M.M. and Pasloske,B.L.						
TITLE	Ribonuclease resistant viral RNA standards						
JOURNAL	Patent: US 5677124-A 8 14-OCT-1997;						
FEATURES	1. .24 /organism="unknown"						
source							
BASE COUNT	6 a	9 c	5 g	4 t			
ORIGIN							
RESULT	14						
A39032	A39032	Sequence 4 from Patent WO9412670.	26 bp	DNA	linear	PAT 05-MAR-1997	
LOCUS							
DEFINITION							
ACCESSION	A39032						
VERSION	A39032.1						
KEYWORDS							
SOURCE	unidentified.						
ORGANISM	unclassified.						
REFERENCE							
AUTHORS	1 (bases 1 to 26)						
TITLE	Maertens,G., Stuyver,L., Rossau,R. and Van,H.H.						
JOURNAL	PROCESS FOR TYPING OF HCV ISOLATES						
COMMENT	patent: WO 9412670-A 4 05-JUN-1994;						
INNOGENETICS NV (BE)							
ACCESSION	Other publication AU 5628294 940622						
VERSION	Other publication CA 2126528 940609						
KEYWORDS	Other publication JP 7503143T 950406.						
SOURCE	Location/Qualifiers						
ORGANISM	Unknown.						
REFERENCE							
AUTHORS	1 (bases 1 to 24)						
TITLE	Lin,L.						
JOURNAL	Nucleic acid preparation methods						
FEATURES	Patent: US 5654119-A 8 05-AUG-1997;						
source	1. .24 /organism="unknown"						
BASE COUNT	7 a	10 c	5 g	4 t			
ORIGIN							
RESULT	15						
AR063366	Query Match	100.0%	Score 24; DB 6;	Length 24;			
Best Local Similarity	100.0%	Score 24;	DB 6;	Length 24;			
Matches	24;	Conservative	0;	Mismatches 0;			
ORIGIN							

	JOURNAL	PATENT:	EP 0905258-A 4 31-MAR-1999;
	FEATURES	INNOGENETICS NV (BE)	Location/Qualifiers
LOCUS	AR063366	from patent US 5846704.	DNA linear PAT 29-SEP-1999
DEFINITION	Sequence 4		
ACCESSION	AR063366		
VERSTON	AR063366.1	GI:5992674	
KEYWORDS	Unknown.		
SOURCE	Organism: Unclassified.		
REFERENCE	1. (bases 1 to 26)		
AUTHORS	Maertens,G., Stuyver,L., Rossau,R. and van Heuverswyn,H.		
TITLE	Process for typing of HCV isolates		
JOURNAL	PATENT: US 5846704-A 4 08-DEC-1998;		
FEATURES	Location/Qualifiers		
SOURCE	1. .26		
BASE COUNT	7 a /organism="unknown"	10 c 5 g 4 t	
ORIGIN			
RESULT 16			
LOCUS	AR123557	26 bp	DNA linear PAT 16-MAY-2001
DEFINITION	Sequence 4 from patent US 6171784.		
ACCESSION	AR123557		
VERSION	AR123557.1	GI:14108918	
KEYWORDS	Unknown.		
SOURCE	Organism: Unclassified.		
REFERENCE	1. (bases 1 to 26)		
AUTHORS	Maertens,G., Stuyver,L., Rossau,R. and van Heuverswyn,H.		
TITLE	Process for typing of HCV isolates		
JOURNAL	PATENT: US 6171784-A 4 09-JAN-2001;		
FEATURES	Location/Qualifiers		
SOURCE	1. .26		
BASE COUNT	7 a /organism="unknown"	10 c 5 g 4 t	
ORIGIN			
RESULT 17			
LOCUS	AX023094	26 bp	DNA linear PAT 20-SEP-2000
DEFINITION	Sequence 4 from Patent EP0905258.		
ACCESSION	AX023094		
VERSION	AX023094.1	GI:10046559	
KEYWORDS	Hepatitis C virus.		
SOURCE	Hepatitis C virus.		
ORGANISM	Hepatitis C virus		
VIRUSES	Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;		
HEPACIVIRUS	Hepacivirus.		
REFERENCE	1. (bases 1 to 26)		
AUTHORS			
TITLE	Method for detecting nucleic acid sequences based on the use of solid phase immobilised nucleotide probes (line probe assay);		
RESULT 19			
LOCUS	I22160	26 bp	DNA linear PAT 07-OCT-1996
DEFINITION	Sequence 19 from patent US 5527669.		

COMMENT	OS	Artificial Sequence	FEATURES	Location/Qualifiers
	PN	JP 2000219200-A/6	SOURCE	1. .33
	PD	10-OCT-2000	BASE COUNT	8 a 12 c 9 g 4 t
	PF	03-FEB-2000 JP 2000032656	ORIGIN	
	PR	03-FEB-1999 US 60/118497		
JEFFREY M LYNN, KEVIN M GORMAN	PC	C12N15/09 // (C12N15/09, C12R1:92), C12N15/00, (C12N15/00,	Query Match	100.0%; Score 24; DB 6; Length 33;
	CC	C12R1:92)	Best Local Similarity	100.0%; Pred. No. 0.00032;
KEY source	FH	Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Indels	
1. .27	FT	1. .27	Gaps	
Location/Qualifiers	FEATURES	/organism="Artificial Sequence".		
/organism="synthetic construct"	SOURCE	/db_xref="taxon:32630"		
BASE COUNT	8 a 10 c 5 g 4 t			
ORIGIN				
Query Match	QY	1 ctgcgaagcacctatcaggagt 24	Query Match	100.0%; Score 24; DB 6; Length 33;
Best Local Similarity	1 ctgcgaagcacctatcaggagt 24	100.0%; Pred. No. 0.00033;	Best Local Similarity	100.0%; Pred. No. 0.00032;
Matches 24; Conservative	0; Mismatches 0; Indels 0; Gaps 0;	Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Mismatches	
QY	Db	3 CTGCAGCACCTATCAGGAGT 26	QY	1 ctgcgaagcacctatcaggagt 24
RESULT 24	AR094974	AR094974 28 bp DNA linear PAT 08-SEP-2000	LOCUS	AR064936 33 bp DNA linear PAT 29-SEP-1999
REFERENCE	1	{bases 1 to 28}	DEFINITION	Sequence 61 from patent US 5849481.
AUTHORS	Wands, J.R., Wakita, T. and Moradpour, D.		ACCESSION	AR064936
TITLE	Antisense inhibition of hepatitis C virus		VERSION	AR064936.1 GI:5995152
FEATURES	JOURNAL	AR094974 Patent: US 6001990-A 12-14-DEC-1999;	KEYWORDS	
source	1. .28	Location/Qualifiers		
KEYWORDS	RESULT 24	/organism="unknown"	JOURNAL	Nucleic acid hybridization assays employing large comb-type branched polynucleotides
SOURCE	AR094974		FEATURES	Patent: US 5849481-A 61-15-DEC-1998;
ORGANISM	Unclassified.		SOURCE	Location/Qualifiers 1. .33
REFERENCE	1	{bases 1 to 28}	BASE COUNT	8 a 12 c 9 g 4 t
AUTHORS	Wands, J.R., Wakita, T. and Moradpour, D.		ORIGIN	
TITLE	Antisense inhibition of hepatitis C virus			
FEATURES	JOURNAL	AR094974 Patent: US 6001990-A 12-14-DEC-1999;	RESULT 27	
source	1. .28	Location/Qualifiers	AR097189 33 bp DNA linear PAT 14-FEB-2001	
BASE COUNT	8 a 11 c 5 g 4 t		LOCUS	AR097189
ORIGIN			DEFINITION	Sequence 127 from patent US 6071693.
RESULT 25	AR04397	AR04397 33 bp DNA linear PAT 04-DEC-1998	ACCESSION	AR097189
REFERENCE	1	{bases 1 to 33}	VERSION	AR097189.1 GI:12805919
AUTHORS	Cha, T., Beall, E., Irvine, B., Kolberg, J. and Urdea, M.S.		KEYWORDS	
TITLE	HCV genomic sequences for diagnostics and therapeutics		SOURCE	
FEATURES	JOURNAL	US 6071693-A 127-06-JUN-2000;	ORGANISM	
source	1. .33	Location/Qualifiers		
BASE COUNT	8 a 12 c 9 g 4 t		BASE COUNT	8 a 12 c 9 g 4 t
ORIGIN			ORIGIN	
Query Match	QY	1 ctgcgaagcacctatcaggagt 24	Query Match	100.0%; Score 24; DB 6; Length 33;
Best Local Similarity	1 ctgcgaagcacctatcaggagt 24	100.0%; Pred. No. 0.00032;	Best Local Similarity	100.0%; Pred. No. 0.00032;
Matches 24; Conservative	0; Mismatches 0; Indels 0; Gaps 0; Oligo 0;	Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Mismatches	
QY	Db	2 CTGCAGCACCTATCAGGAGT 25	QY	1 ctgcgaagcacctatcaggagt 24
RESULT 25	AR04397	AR04397 33 bp DNA linear PAT 04-DEC-1998	LOCUS	
REFERENCE	1	{bases 1 to 33}	DEFINITION	
AUTHORS	Sheridan, P., Chang, C.-A., Running, J. and Urdea, M.S.		ACCESSION	
TITLE	Nucleic acid probes immobilized on polystyrene surfaces		VERSION	
FEATURES	JOURNAL	Patent: US 5747244-A 51-05-MAY-1998;	KEYWORDS	
source	1. .33	Location/Qualifiers		
BASE COUNT	8 a 12 c 9 g 4 t		BASE COUNT	8 a 12 c 9 g 4 t
ORIGIN			ORIGIN	
Query Match	QY	1 ctgcgaagcacctatcaggagt 24	Query Match	100.0%; Score 24; DB 6; Length 33;
Best Local Similarity	1 ctgcgaagcacctatcaggagt 24	100.0%; Pred. No. 0.00032;	Best Local Similarity	100.0%; Pred. No. 0.00032;
Matches 24; Conservative	0; Mismatches 0; Indels 0; Gaps 0; Oligo 0;	Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Mismatches	

	TITLE	Solution phase nucleic acid sandwich assays having reduced background noise
VERSION	AX284180.1	GI:17044868
KEYWORD	synthetic construct.	
SOURCE	synthetic construct	
ORGANISM	artificial sequence.	
REFERENCE	1 (sites)	
AUTHORS	Farudi,A.F.	
TITLE	Detection and amplification or rna using target-mediated ligation of dna by rna ligase	
JOURNAL	Patent: WO 0179420-A 1 25-OCT-2001;	
FEATURES	MOLECULAR STAGING, INC. (US)	
source	Location/Qualifiers 1. .47 /organism="synthetic construct" /db xref="taxon:32630" /note="Synthetic Target".	
BASE COUNT	7 a	
ORIGIN	11 c 18 g 11 t	
RESULT	33	
Query Match	100.0%; Score 24; DB 6; Length 47;	
DEFINITION	Best Local Similarity 100.0%; Pred. No. 0.0003; Mismatches 24; Conservative 0; Indels 0; Gaps 0;	
ACCESSION	QY 1 ctgcgaagcacctatcaggcagt 24	
VERSION	Db 39 CTCGCAAGCACCTATCAGGCAGT 16	
SOURCE	Unknown.	
ORGANISM	Unclassified.	
REFERENCE	1 (bases 1 to 53)	
AUTHORS	Urdea,M.S., Fultz,T., Warner,B.D. and Collins,M.	
TITLE	Solution phase nucleic acid sandwich assays having reduced background noise	
JOURNAL	Patent: US 5635352-A 16 03-JUN-1997;	
FEATURES	Location/Qualifiers 1. .53 /organism="unknown"	
BASE COUNT	12 a 17 c 15 g 9 t	
ORIGIN		
RESULT	35	
Query Match	100.0%; Score 24; DB 6; Length 53;	
DEFINITION	Best Local Similarity 100.0%; Pred. No. 0.00029; Mismatches 24; Conservative 0; Indels 0; Gaps 0;	
ACCESSION	QY 1 ctgcgaagcacctatcaggcagt 24	
VERSION	Db 27 CTCGCAAGCACCTATCAGGCAGT 50	
SOURCE	Unknown.	
ORGANISM	Unclassified.	
REFERENCE	1 (bases 1 to 53)	
AUTHORS	Urdea,M.S., Fultz,T., Warner,B.D. and Collins,M.	
TITLE	Solution phase nucleic acid sandwich assays having reduced background noise and kits therefor	
JOURNAL	Patent: US 5681697-A 16 28-OCT-1997;	
FEATURES	Location/Qualifiers 1. .53 /organism="unknown"	
BASE COUNT	12 a 17 c 15 g 9 t	
ORIGIN		
RESULT	36	
Query Match	100.0%; Score 24; DB 6; Length 53;	
DEFINITION	Best Local Similarity 100.0%; Pred. No. 0.00029; Mismatches 24; Conservative 0; Indels 0; Gaps 0;	
ACCESSION	QY 1 ctgcgaagcacctatcaggcagt 24	
VERSION	Db 27 CTCGCAAGCACCTATCAGGCAGT 50	
SOURCE	Unknown.	
ORGANISM	Unclassified.	
REFERENCE	1 (bases 1 to 53)	
AUTHORS	Urdea,M.S., Fultz,T., Warner,B.D. and Collins,M.	
TITLE	Solution phase nucleic acid sandwich assays having reduced background noise and kits therefor	
JOURNAL	Patent: US 5681697-A 19 28-OCT-1997;	
FEATURES	Location/Qualifiers 1. .53 /organism="unknown"	
BASE COUNT	12 a 17 c 15 g 9 t	
ORIGIN		
RESULT	34	
Query Match	100.0%; Score 24; DB 6; Length 53;	
DEFINITION	Best Local Similarity 100.0%; Pred. No. 0.00029; Mismatches 24; Conservative 0; Indels 0; Gaps 0;	
ACCESSION	QY 1 ctgcgaagcacctatcaggcagt 24	
VERSION	Db 27 CTCGCAAGCACCTATCAGGCAGT 50	
SOURCE	Unknown.	
ORGANISM	Unclassified.	
REFERENCE	1 (bases 1 to 53)	
AUTHORS	Urdea,M.S., Fultz,T., Warner,B.D. and Collins,M.	
TITLE	Solution phase nucleic acid sandwich assays having reduced background noise and kits therefor	
JOURNAL	Patent: US 5681697-A 19 28-OCT-1997;	
FEATURES	Location/Qualifiers 1. .53 /organism="unknown"	
BASE COUNT	12 a 17 c 15 g 9 t	
ORIGIN		
RESULT	34	
Query Match	100.0%; Score 24; DB 6; Length 53;	
DEFINITION	Sequence 49 from patent US 5635352.	
ACCESSION	I44620	
VERSION	I44620.1 GI:246933	
SOURCE	Unknown.	
ORGANISM	Unclassified.	
REFERENCE	1 (bases 1 to 53)	
AUTHORS	Urdea,M.S., Fultz,T., Warner,B.D. and Collins,M.	
TITLE	Solution phase nucleic acid sandwich assays having reduced background noise	
JOURNAL	Patent: US 5635352-A 16 03-JUN-1997;	
FEATURES	Location/Qualifiers 1. .53 /organism="unknown"	
BASE COUNT	12 a 17 c 15 g 9 t	
ORIGIN		

REFERENCE	1 (bases 1 to 64)	ORIGIN	
AUTHORS	Urdea,M.S., Fultz,T., Warner,B.D. and Collins,M.	TITLE	Solution phase nucleic acid sandwich assays having reduced background noise and kits therefor
JOURNAL	Patent: US 5681697-A 31-28-OCT-1997;	FEATURES	Location/Qualifiers
source	1..64	/organism="unknown"	BASE COUNT
BASE COUNT	18 a 16 c	17 g	13 t
ORIGIN			
RESULT	42	Query Match	100.0%; Score 24; DB 6; Length 64; Best Local Similarity 100.0%; Pred. No. 0.0028; Mismatches 0; Indels 0; Gaps 0;
LOCUS	AX021668/c	DEFINITION	Sequence 47 from Patent WO99/3250.
ACCESSION	AX021668	VERSION	AX021668.1 GI:1044951
KEYWORDS			
SOURCE			
ORGANISM	Hepatitis C virus.	VIRUSES	Heptatitis C viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae; Hepacivirus.
REFERENCE	1 (bases 1 to 75)	AUTHORS	Kessler,C., Bartl,K., Haberhausen,G. and Orum,H.
TITLE	Specific and sensitive method for detecting nucleic acids	JOURNAL	
JOURNAL	Patent: WO 932350-A 47-14-MAY-1999;	FEATURES	
FEATURES	KESSLER CHRISTOPH (DE); BARTL KURT (DE); HABERHAUSEN GERD (DE); ROCHE DIAGNOSTICS GMBH (DE); ORUM HENRIK (DK)	source	1..75 '/organism="Hepatitis C virus" '/db_xref="taxon:11103"
BASE COUNT	13 a 20 c	ORIGIN	25 g 17 t
RESULT	44	Query Match	100.0%; Score 24; DB 6; Length 64; Best Local Similarity 100.0%; Pred. No. 0.0028; Mismatches 0; Indels 0; Gaps 0;
LOCUS	I22161	DEFINITION	Sequence 20 from patent US 5527669.
ACCESSION	I22161	VERSION	I22161.1 GI:1602515
KEYWORDS			
SOURCE		ORGANISM	Unknown.
REFERENCE	Unclassified.	AUTHORS	Resnick,R.M. and Young,K.K.Y.
TITLE	Methods, primers and probes for detection of hepatitis C and novel variants	JOURNAL	Patent: US 5527669-A 20-18-JUN-1995;
JOURNAL		FEATURES	Location/Qualifiers
FEATURES	Location/Qualifiers	source	1..29 '/organism="unknown"
BASE COUNT	8 a 8 c	ORIGIN	8 g 5 t
RESULT	44	Query Match	95.8%; Score 23; DB 6; Length 29; Best Local Similarity 100.0%; Pred. No. 0.0014; Mismatches 0; Indels 0; Gaps 0;
LOCUS	I22161	DEFINITION	Sequence 23; Conservative
ACCESSION	I22161	VERSION	I22161.1 GI:1602515
KEYWORDS			
SOURCE		ORGANISM	Unknown.
REFERENCE	Unclassified.	AUTHORS	Marschall,R.L., Carrino,J.J. and Sustachek,J.C.
TITLE	Amplification of RNA sequences using the ligase chain reaction	JOURNAL	Patent: US 5686272-A 27-11-NOV-1997;
JOURNAL		FEATURES	Location/Qualifiers
FEATURES	Location/Qualifiers	source	1..22 '/organism="unknown"
BASE COUNT	3 a 4 c	ORIGIN	9 g 6 t
RESULT	45	Query Match	91.7%; Score 22; DB 6; Length 22; Best Local Similarity 100.0%; Pred. No. 0.0061; Mismatches 0; Indels 0; Gaps 0;
LOCUS	I73296	DEFINITION	Sequence 27 from patent US 5686272.
ACCESSION	I73296	VERSION	I73296.1 GI:3009435
KEYWORDS			
SOURCE		ORGANISM	Unknown.
REFERENCE	Unclassified.	AUTHORS	Marschall,R.L., Carrino,J.J. and Sustachek,J.C.
TITLE	Amplification of RNA sequences using the ligase chain reaction	JOURNAL	Patent: US 5686272-A 27-11-NOV-1997;
JOURNAL		FEATURES	Location/Qualifiers
FEATURES	Location/Qualifiers	source	1..22 '/organism="unknown"
BASE COUNT	3 a 4 c	ORIGIN	9 g 6 t
RESULT	45	Query Match	91.7%; Score 22; DB 6; Length 22; Best Local Similarity 100.0%; Pred. No. 0.0061; Mismatches 0; Indels 0; Gaps 0;
LOCUS	I73296	DEFINITION	Sequence 27 from patent US 5686272.
ACCESSION	I73296	VERSION	I73296.1 GI:3009435
KEYWORDS			
SOURCE		ORGANISM	Unknown.
REFERENCE	Unclassified.	AUTHORS	Marschall,R.L., Carrino,J.J. and Sustachek,J.C.
TITLE	Amplification of RNA sequences using the ligase chain reaction	JOURNAL	Patent: US 5686272-A 27-11-NOV-1997;
JOURNAL		FEATURES	Location/Qualifiers
FEATURES	Location/Qualifiers	source	1..23 '/organism="unknown"
BASE COUNT	6 a 8 c	ORIGIN	5 g 4 t

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Page 12

Search completed: August 26, 2002, 21:20:54
Job time: 7708 sec

SQ	sequence	24	BP;	6	A;	9	C;	5	G;	4	T;	0	other;	Qy	1	ctcgcaagccctatcaggcagt	24
Query Match		100	0%	Score	24;	DB	16;	Length	24;								
Best Local Similarity		100	0%	Pred.	No.	4.4e-05;											
Matches		24;	Conservative					Mismatches	0;	Indels	0;	Gaps	0;	RESULT	5		
Db		1	ctcgcaagccctatcaggcagt	24										ID	AAT93542	AAT93542	standard; DNA; 24
RESULT	4													ID	AAT93542	AAT93542	standard; DNA; 24
ID	AAT64900		standard;	DNA;	24	BP.								XX			
XX														AC	AAT93542;		
AC	AAT64900;													XX			
XX														DT	19-FEB-1998	(first entry)	
DT	12-MAR-1998		(first entry)											XX			
XX														DE	Antisense primer KY78 for amplification of HCV RNA.		
DE	Hepatitis C virus (HCV) oligonucleotide KY78.													XX			
XX														KW	Armoured RNA; bacteriophage MS2; RT-PCR; ribonuclease; recombinant;		
KW														KW	Human Immunodeficiency virus; HIV; HCV; Viral RNA;		
KW														KW	detection; quantification standard; matruse protein; coat protein;		
KW														KW	PCR primer; QS RNA; reverse transcriptase-PCR; ss.		
KW														XX			
KW														OS	Synthetic.		
OS														OS	Hepatitis C virus.		
OS														XX			
OS														XX			
OS														PN	US567124-A.		
OS														XX			
OS														PD	14-OCT-1997.		
OS														XX			
OS														PF	03-JUL-1996;	96US-0675153.	
OS														XX			
OS														PR	03-JUL-1996;	96US-0675153.	
OS														XX			
OS														PA	(AMBI-) AMBION INC.		
OS														PA	(CENFE-) CENETRON DIAGNOSTICS LLC.		
OS														XX			
OS														PI	Dubois DB, Pasloske BL, Winkler MM;		
OS														XX			
OS														DR			
OS														XX			
OS														PA			
OS														XX			
OS														PA			
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OS																	

DE HCV gene PCR primer KY78.
 XX
 KW RNA; plasma; hepatitis C virus; HCV; primer; PCR;
 XX polymerase chain reaction; ss.
 XX OS Synthetic.
 XX US5654179-A.
 XX PD 05-AUG-1997.
 XX PF 14-NOV-1990; 90US-0614921.
 XX PR 08-APR-1993; 93US-0044649.
 XX PR 14-NOV-1990; 90US-0614921.
 XX PR 19-JUN-1992; 92US-0901545.
 XX PR 03-OCT-1994; 94US-0317220.
 PA (HYDS) HRI RES INC.
 XX Lin L; PI
 XX DR WPI; 1997-401849/37.
 PT Preparation of RNA samples from plasma - by alcohol precipitation after lysis with guanidinium thiocyanate
 XX Disclosure; Column 47; 60pp; English.
 XX PS
 CC Primer KY78 (AAT87095) and primer KY80 (AAT87096) were used for the PCR amplification of a 305 bp hepatitis C virus gene product (see AAT87088). A claimed method for preparing RNA samples comprises: (a) mixing plasma with an aqueous buffer solution containing guanidinium thiocyanate and beta-mercaptoethanol; (b) heating the mixture; (c) adding an equal volume of an alcohol to precipitate RNA; and (d) recovering the RNA. The method can be used to prepare RNA samples for subsequent amplification, especially for detecting pathogens, e.g., hepatitis C virus or HIV. Compared with the known "IsoQuick" and "RNazol" methods, the method uses fewer tubes (just one), requires fewer steps, takes less time and produces no toxic waste.
 XX Sequence 24 BP; 6 A; 9 C; 5 G; 4 T; 0 other;
 Query Match 100 %; Score 24; DB 18; Length 24;
 Best Local Similarity 100 %; Pred. No. 4.4e-05; Mismatches 0;
 Matches 24; Conservative 0; Indels 0; Gaps 0;
 QY 1 ctgcgaagcccttatcaggcgt 24
 Db 1 ctgcgaagcccttatcaggcgt 24
 RESULT 8
 ID AAV15119
 ID AAV15119 standard; DNA; 24 BP.
 AC AAV15119;
 AC AAV15119;
 XX DT 28-MAY-1998 (first entry)
 XX DE Hepatitis C virus PCR primer PKY78.
 XX KW Hepatitis C virus; HCV; PCR primer; detection; reverse transcription; enzyme immunoassay; viral RNA; ss.
 XX OS Synthetic.
 XX OS Hepatitis C virus.
 XX PN WO9746716-A1.
 XX PD 11-DEC-1997.
 XX PR 03-JUN-1997; 97WO-IT00128.
 XX PR 07-JUN-1996; 96IT-M000404.
 XX PA (WESA) WABCO BV.
 XX PI Bosio P, Clemenza F, Strumia C;
 XX DR WPI; 1998-042222/04.
 XX PT Detection of hepatitis C virus - by reverse transcription, single-step PCR and detection by DNA enzyme immunoassay
 XX Disclosure; Page 4; 26pp; English.

XX
CC The present sequence represents a PCR primer involved in the method of
CC the present invention for detecting hepatitis C virus (HCV). The method
CC comprises: (a) reverse-transcribing the viral RNA; (b) amplifying the
CC resulting cDNA by a single polymerase chain reaction in a reaction
mixture having a Mg²⁺/Taq polymerase ratio of about 100 n mole/enzyme
unit; and (c) detecting the amplification product by DEIA (DNA enzyme
immunoassay) using an Oligonucleotide probe. The sensitivity of this
method is at least equal to that achievable by more complicated assays
CC using nested PCR.
CC
XX Sequence 24 BP; 6 A; 9 C; 5 G; 4 T; 0 other;
SQ

Query Match Similarity 100.0%; Score 24; DB 19; Length 24;
Best Local Similarity 100.0%; Pred. No. 4.4e-05;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ctcccaaaacccatcgccgacgt 24
Db 1 ctccgaaggaccatcatcgccgact 24

RESULT 9
AAZ09798
ID AAZ09798 standard; DNA; 24 BP.
XX
AC
XX
DT 26-NOV-1999 (first entry)
DE HCV PCR primer KY78.
XX
KW Probe; amplification; primer; reporter group; quencher group; PCR;
KW amplicon; detection; ss.
XX
OS Synthetic.
OS Hepatitis C virus.
XX
PN DE19814001-A1.
XX
PD 30-SEP-1999.
XX
PF 28-MAR-1998; 98DE-1014001.
XX
PR 28-MAR-1998; 98DE-1014001.
XX
PA (HOFF) ROCHE DIAGNOSTICS GMBH.
XX
PT Kessler C, Haberhausen G, Batz H, Orum H.
XX
DR WPI; 1999-552213/47.

XX
PT Fluorescent nucleic acid amplification assay, useful for detection of
viral, bacterial, cellular, yeast or fungal nucleic acids
XX
PS Example 1; Page 19; 16pp; German.
XX
CC This invention describes a novel assay for a nucleic acid which comprises
an amplification reaction using two non-overlapping primers, a polymerase
with 5' nuclelease activity and a probe with reporter groups and quencher
groups that binds a region other than that bound by the primers. The assay is
reaction generates products of less than 100 nucleotides. The assay is
useful for detection of viral, bacterial, cellular, yeast or fungal
nucleic acids in human, animal, bacterial, plant, yeast or fungal
samples, e.g., feces, smears, cell suspensions, cultures or tissue, cell
or liquid biopsy samples. Compared with assays in which longer
amplicon products are generated, the assay can be performed more
rapidly using shorter polymerase chain reaction (PCR) cycles, sensitivity
may be increased due to reduced competition between the short
counterstrand of the amplicon and the detector probe. Specificity may
also be increased because of the increased relative length of sequence B
compared with the total length of the amplicon and the differentiability

CC of subtypes may be increased. In addition signal-to-noise ratios may be
CC increased with the new method because short amplicons have reduced
CC potential for nonspecific hybridization. In addition reproducibility may
be increased because small target regions on RNA genomes are less
sensitive to RNA degradation, and the possibilities for secondary
structure formation are reduced. This sequence represents a PCR primer
CC used in the amplification of a region of HCV which is used to illustrate
CC the method of the invention.
CC
XX Sequence 24 BP; 6 A; 9 C; 5 G; 4 T; 0 other;
SQ

Query Match Similarity 100.0%; Score 24; DB 20; Length 24;
Best Local Similarity 100.0%; Pred. No. 4.4e-05;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ctgcgaaggaccatcatcgccgact 24
Db 1 ctccgaaggaccatcatcgccgact 24

RESULT 10
AX7452
ID AX7452 standard; DNA; 24 BP.
XX
AC
XX
DT 26-AUG-1999 (first entry)
DE HCV PCR primer 2.
XX
KW RNA standard; HCV; detection; gag gene; cerebrospinal fluid; PCR primer;
KW ribonuclease resistant; encapsulation; viral; HIV-1; HIV-2; HCV;
KW HTLV-1; HTLV-2; hepatitis G; enterovirus; blood-borne pathogen; ss.
OS Synthetic.
OS Hepatitis C virus.
XX
PN US5919625.A.
XX
PD 06-JUL-1999.
XX
PF 29-APR-1997; 97US-0841252.
XX
PR 03-JUL-1996; 96US-0675153.
PR 29-APR-1997; 97US-0841252.
XX
PA (AMBI-) AMBION INC.
PA (CEN-) CENETRON DIAGNOSTICS LLC.
XX
PT Dubois DB, Pasloske BL, Winkler MM;
XX
DR WPI; 1999-394617/33.
XX
PT Ribonuclease resistant viral RNA standards
XX
PS Example V; Column 31-32; 22pp; English.

XX
CC This invention describes the construction of novel RNA standards for the
quantification of human immunodeficiency virus (HIV) and hepatitis C
virus (HCV) from e.g. cerebrospinal fluids. The method involves (1)
obtaining a sample to be analysed; (2) obtaining a ribonuclease resistant
RNA standard, encapsulated in a bacteriophage viral coat protein, which
comprises an RNA segment having a segment encoding a sequence that serves
as a standard in detection or quantification of the RNA of interest;
CC (3) mixing the sample with the standard; (4) isolating RNA from the
mixture, and (5) assaying for the presence of the RNA. The method is
useful for the detection or quantification of HIV-1, HIV-2, HCV, HTLV-1,
HTLV-2, hepatitis G, an enterovirus, or a blood borne Pathogen. This
sequence represents a PCR primer used to amplify a region of the
CC Hepatitis C genome which is used in the method of the invention.
CC
XX Sequence 24 BP; 6 A; 9 C; 5 G; 4 T; 0 other;

DE PCR primer used to amplify a HCV DNA fragment.
 XX
 KW Magnetic glass particle; nucleic acid purification; PCR primer; ss.
 XX
 OS Hepatitis C virus.
 XX
 PN WO200137291-A1.
 XX
 PD 25-MAY-2001.
 XX
 PF 17-NOV-2000; 2000WO-EP11459.
 XX
 PR 17-NOV-1999; 99EP-0122053.
 PR 12-MAY-2000; 2000EP-0110165.
 XX
 PA (HOFF) ROCHE DIAGNOSTICS GMBH.
 XX
 PI Weindel K, Riedling M, Geiger A;
 DR WPI; 2001-381247/40.
 XX
 PT Novel composition of magnetic glass particles for purification of DNA
 PT or RNA in automated processes
 XX
 PS Example 7; Page 95; 105PP; English.

XX
 CC The specification describes a composition of magnetic glass particles,
 CC which contain at least one magnetic object with a mean diameter between
 CC 5-500 nm. The composition is useful for the purification of nucleic
 acids. The composition can be used to process large quantities of
 nucleic acid samples, because it does not involve the particles being
 centrifuged or the fluids being drawn through glass fiber filters.
 CC PCR primers AAH25403-04 were used to amplify HCV DNA fragments. The
 CC amplified fragment can be purified using the method of the invention.
 XX
 SQ Sequence 24 BP; 6 A; 9 C; 5 G; 4 T; 0 other;

XX
 CC Query Match 100.0%; Score 24; DB 22; Length 24;
 CC Best Local Similarity 100.0%; Pred. No. 4.4e-05;
 CC Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 CC Qy 1 ctgcgaagccctatcaggcagt 24
 CC Db 1 ctgcgaagccctatcaggcagt 24
 XX
 SQ Sequence 26 BP; 7 A; 10 C; 5 G; 4 T; 0 other;

XX
 CC Query Match 100.0%; Score 24; DB 14; Length 26;
 CC Best Local Similarity 100.0%; Pred. No. 4.4e-05;
 CC Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 CC Qy 1 ctgcgaagccctatcaggcagt 24
 CC Db 3 ctgcgaagccctatcaggcagt 26
 XX
 SQ Sequence 26 BP; 7 A; 10 C; 5 G; 4 T; 0 other;

RESULT 14

ID	Query	Match	Score	DB	Length	Similarity	Pred. No.	Mismatches	Indels	Gaps
AAQ37587	ctcgaaagccctatcaggcagt	ctcgaaagccctatcaggcagt	24	24	24	100.0%	4.4e-05	0	0	0
AAQ37587	1	1								

XX
 AC AAQ37587;
 XX
 DT 23-JUN-1993 (first entry)

XX
 DE HCV conserved region downstream primer/probe KY145, position 276-301.
 XX
 KW Polymerase chain reaction; PCR; amplify; primer; probe; hepatitis C;
 KW virus; HCV; conserved region; RNA; open reading frame; polyprotein;
 KW prototype; untranslated region; UTR; 5'UTR; conserved; replication;
 KW regulation; US; Japan; C9; ss.
 XX
 OS Synthetic.
 XX
 PN EP529493-A.
 XX
 PD 03-MAR-1993.
 XX
 PF 19-AUG-1992; 92EP-0114115.
 XX
 PR 27-AUG-1991; 91US-0751305.
 PR 21-JUL-1992; 92US-0918844.

RESULT 15

ID	Query	Match	Score	DB	Length	Similarity	Pred. No.	Mismatches	Indels	Gaps
AAQ68061	ctcgaaagccctatcaggcagt	ctcgaaagccctatcaggcagt	24	26	26	100.0%	4.4e-05	0	0	0
AAQ68061	1	1								

XX
 AC AAQ68061;
 XX
 DT 19-DEC-1994 (first entry)

DE Primer HcPr96 for HCV genotyping (universal).

XX
 KW Hepatitis C virus; HCV; probe; genotyping; hybridisation;
 KW non-A, non-B hepatitis; NANBH; amplification; primer;
 KW polymerase chain reaction; PCR; ss.
 XX
 OS Synthetic.
 XX
 PN WO9412670-A.
 XX
 PD 09-JUN-1994.
 XX
 PF 26-NOV-1993; 93WO-EP03325.
 XX
 PR 27-NOV-1992; 92EP-0403222.
 PR 31-AUG-1993; 93EP-0402129.
 XX
 PA (INNO-) INNOGENETICS NV SA.
 XX
 PI Maertens G, Rossau R, Stuyver L, Van Heuverswyn H;
 XX
 DR WPI; 1994-200296/24.
 XX
 PT Processes for genotyping Hepatitis C virus (HCV) isolates -
 PT utilises probes hybridising to HCV isolate domains
 XX
 PS Claim 13; Page 73; 96pp; English.

CC Genotyping HCV utilises probes hybridising to HCV isolate domains.
 CC HCV types 2, 3, 4, 5 or 6 and subtypes 1a, 1b, 2a, 2b, 3a, 3b,
 CC 3c, 4a, 4b, 4c, 4f, 4g can be typed.
 CC The hybridisation step is pref. preceded by an amplification
 CC step (PCR) using universal primers given in AAQ68058-61.
 XX SQ Sequence 26 BP; 7 A; 10 C; 5 G; 4 T; 0 other;

Query Match 100.0%; Score 24; DB 15; Length 26;
 Best Local Similarity 100.0%; Pred. No. 4.4e-05; Length 26;

Mismatches 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ctcgcagaagccatctacggcgt 24
 ||||||| ||||||| ||||||| |||||||
 Db 3 ctgcgaagccatctacggcgt 26

RESULT 17
 AAZ57408 Query Match 100.0%; Score 24; DB 18; Length 26;
 ID AAZ57408 standard; DNA; 26 BP.

XX ID AAZ57408;

AC AC AAZ57408;

XX DT 07-APR-2000 (first entry)

XX Hepatitis C virus PCR primer A5'-TT SEQ ID NO:23.

XX Hepatitis C virus; RNA virus; replication; viral infection;

KW PCR primer; ss.

XX OS Hepatitis C virus.

XX PN WO9967394-A1.

XX PD 29-DEC-1999.

XX PF 24-JUN-1999; 99WO-JP03380.

XX PR 24-JUN-1998; 98JP-0177820.

XX PA (CHUS) CHUGAI SEIYAKU KK.

XX PI Kohara M, Kohara K, Taira K, Matsuzaki J, Ohmori H;

XX DR WPI; 2000-106296/09.

XX PS Example 2; Page 21; 46pp; Japanese.

XX The present invention describes a vector comprising a cDNA encoding an

CC RNA virus gene, constructed to ensure the exact and homogeneous

CC transcription of both terminals of the RNA virus gene. Also described

CC is a method for screening drugs for inhibiting the replication of RNA

CC virus by using the RNA viral infection model animal, particularly one

CC with hepatitis C viral infection. The vector is useful in clarifying

CC the mechanism of RNA viral replication, onset of RNA viral infection,

CC and developing remedies and therapeutics for RNA viral infections,

CC particularly of a hepatitis C virus. The present sequence represents

CC a PCR primer which is used in the exemplification of the present

CC invention.

XX SQ Sequence 26 BP; 7 A; 10 C; 5 G; 4 T; 0 other;

Query Match 100.0%; Score 24; DB 21; Length 26;

Best Local Similarity 100.0%; Pred. No. 4.4e-05; Length 26;

Mismatches 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ctcgcagaagccatctacggcgt 24
 ||||||| ||||||| ||||||| |||||||
 Db 3 ctgcgaagccatctacggcgt 26

RESULT 18

AAQ71839 Query Match 100.0%; Score 24; DB 18; Length 26;

ID AAQ71839 standard; DNA; 27 BP.

XX

Sequence 26 BP; 7 A; 10 C; 5 G; 4 T; 0 other;

XX

This oligonucleotide KY145 can be used as a probe for detecting

CC hepatitis C virus (HCV) nucleic acid from a Japanese or US prototype

CC strain as well as HCV C9 prototype strain. This oligonucleotide can

CC also be used as a primer for amplifying HCV nucleic acid. The sequence

CC of this oligonucleotide is contained in a specific region of HCV genomic

CC nucleic acid. The probe or the primer is preferably labelled. The probe

CC is used to detect HCV nucleic acid, preferably after this has been

CC amplified using the new primer in reverse transcription polymerase chain

CC reaction (RT-PCR), for both diagnostic and epidemiological applications.

CC The primer is effective for both reverse transcription and PCR,

CC eliminating the need to open the reaction tube during the procedure.

CC Amplification is effective (no need for a second round of PCR with nested

CC primers) and provides high sensitivity. The probe is directed to

CC conserved regions and so can detect many different strains without loss

CC of specificity.

XX

Sequence 26 BP; 7 A; 10 C; 5 G; 4 T; 0 other;

XX

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XX

Sequence 26 BP; 7 A; 10 C; 5 G; 4 T; 0 other;

XX

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XX

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XX

Sequence 26 BP; 7 A; 10 C; 5 G; 4 T; 0 other;

XX

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CC nucleic acid. The probe or the primer is preferably labelled. The probe

CC is used to detect HCV nucleic acid, preferably after this has been

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CC reaction (RT-PCR), for both diagnostic and epidemiological applications.

CC The primer is effective for both reverse transcription and PCR,

CC eliminating the need to open the reaction tube during the procedure.

CC Amplification is effective (no need for a second round of PCR with nested

CC primers) and provides high sensitivity. The probe is directed to

CC conserved regions and so can detect many different strains without loss

CC of specificity.

XX

Sequence 26 BP; 7 A; 10 C; 5 G; 4 T; 0 other;

XX

This oligonucleotide KY145 can be used as a probe for detecting

CC hepatitis C virus (HCV) nucleic acid from a Japanese or US prototype

CC strain as well as HCV C9 prototype strain. This oligonucleotide can

CC also be used as a primer for amplifying HCV nucleic acid. The sequence

CC of this oligonucleotide is contained in a specific region of HCV genomic

CC nucleic acid. The probe or the primer is preferably labelled. The probe

CC is used to detect HCV nucleic acid, preferably after this has been

CC amplified using the new primer in reverse transcription polymerase chain

CC reaction (RT-PCR), for both diagnostic and epidemiological applications.

CC The primer is effective for both reverse transcription and PCR,

CC eliminating the need to open the reaction tube during the procedure.

CC Amplification is effective (no need for a second round of PCR with nested

CC primers) and provides high sensitivity. The probe is directed to

CC conserved regions and so can detect many different strains without loss

CC of specificity.

XX

Sequence 26 BP; 7 A; 10 C; 5 G; 4 T; 0 other;

XX

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CC hepatitis C virus (HCV) nucleic acid from a Japanese or US prototype

CC strain as well as HCV C9 prototype strain. This oligonucleotide can

CC also be used as a primer for amplifying HCV nucleic acid. The sequence

CC of this oligonucleotide is contained in a specific region of HCV genomic

CC nucleic acid. The probe or the primer is preferably labelled. The probe

CC is used to detect HCV nucleic acid, preferably after this has been

CC amplified using the new primer in reverse transcription polymerase chain

CC reaction (RT-PCR), for both diagnostic and epidemiological applications.

CC The primer is effective for both reverse transcription and PCR,

CC eliminating the need to open the reaction tube during the procedure.

CC Amplification is effective (no need for a second round of PCR with nested

CC primers) and provides high sensitivity. The probe is directed to

CC conserved regions and so can detect many different strains without loss

CC of specificity.

XX

Sequence 26 BP; 7 A; 10 C; 5 G; 4 T; 0 other;

XX

This oligonucleotide KY145 can be used as a probe for detecting

CC hepatitis C virus (HCV) nucleic acid from a Japanese or US prototype

CC strain as well as HCV C9 prototype strain. This oligonucleotide can

CC also be used as a primer for amplifying HCV nucleic acid. The sequence

CC of this oligonucleotide is contained in a specific region of HCV genomic

CC nucleic acid. The probe or the primer is preferably labelled. The probe

CC is used to detect HCV nucleic acid, preferably after this has been

CC amplified using the new primer in reverse transcription polymerase chain

CC reaction (RT-PCR), for both diagnostic and epidemiological applications.

CC The primer is effective for both reverse transcription and PCR,

CC eliminating the need to open the reaction tube during the procedure.

CC Amplification is effective (no need for a second round of PCR with nested

CC primers) and provides high sensitivity. The probe is directed to

CC conserved regions and so can detect many different strains without loss

CC of specificity.

XX

Sequence 26 BP; 7 A; 10 C; 5 G; 4 T; 0 other;

XX

This oligonucleotide KY145 can be used as a probe for detecting

CC hepatitis C virus (HCV) nucleic acid from a Japanese or US prototype

CC strain as well as HCV C9 prototype strain. This oligonucleotide can

CC also be used as a primer for amplifying HCV nucleic acid. The sequence

CC of this oligonucleotide is contained in a specific region of HCV genomic

CC nucleic acid. The probe or the primer is preferably labelled. The probe

CC is used to detect HCV nucleic acid, preferably after this has been

CC amplified using the new primer in reverse transcription polymerase chain

CC reaction (RT-PCR), for both diagnostic and epidemiological applications.

CC The primer is effective for both reverse transcription and PCR,

CC eliminating the need to open the reaction tube during the procedure.

CC Amplification is effective (no need for a second round of PCR with nested

CC primers) and provides high sensitivity. The probe is directed to

CC conserved regions and so can detect many different strains without loss

CC of specificity.

XX

Sequence 26 BP; 7 A; 10 C; 5 G; 4 T; 0 other;

XX

This oligonucleotide KY145 can be used as a probe for detecting

CC hepatitis C virus (HCV) nucleic acid from a Japanese or US prototype

CC strain as well as HCV C9 prototype strain. This oligonucleotide can

CC also be used as a primer for amplifying HCV nucleic acid. The sequence

CC of this oligonucleotide is contained in a specific region of HCV genomic

CC nucleic acid. The probe or the primer is preferably labelled. The probe

CC is used to detect HCV nucleic acid, preferably after this has been

PT	hepatitis C virus in hepatocytes -								
XX									
PS	Example 3; Page 18; 39pp; English.								
CC	The invention relates to a novel process and cell culture medium for in vitro replication of hepatitis C virus (HCV) in primary mammalian hepatocytes. The culture medium comprising one or more mammalian plasma or sera, a chemical or biological compound with an anti-oxidative property and/or a differentiating property, such as dimethyl sulphoxide (DMSO), retinoic acid, vitamin (e.g., vitamin E), or selenium, and/or at least one corticoid. The culture medium may be used in an in vitro HCV infection and culture system. This would allow the mechanisms of viral replication to be studied, and could also be used for in vitro screening of anti-HCV drugs; to test neutralising antibodies; for in vitro diagnosis of HCV; and for the preparation of vaccines against HCV. The HCV-infected hepatocytes survive for at least 4 months in the culture medium. Previously, a reliable and robust in vitro HCV culture method has not been available. Sequences AK287367-287375 represent reverse transcriptase-PCR (RT-PCR) primers used in an exemplification of the present invention.								
CC	AK287367-287375 represent reverse transcriptase-PCR (RT-PCR) primers used in an exemplification of the present invention.								
SQ	Sequence 27 BP; 8 A; 10 C; 5 G; 4 T; 0 other;								
Query	Match	100.0%	Score	24	DB	21	Length	27	
Best	Local Similarity	100.0%	Pred. No.	4.4e-05					
Matches	24	Conservative	0	Mismatches	0	Indels	0	Gaps	0
OY	1	ctcgcaaggccatcatcgcgat	24						
Db	2	ctcgcaaggccatcatcgcgat	25						
RESULT	21								
ID	AB02736	standard; RNA; 27 BP.							
XX	ABA02736;								
XX	ABA02736;								
AC									
XX									
DE	Nucleic acid sensor molecule SEQ ID NO 8.								
XX									
KW	Nucleic acid sensor molecule; detection; infection; disease diagnosis; physiological abnormality; electronic; signalling molecule; nucleoside analogue; ss.								
KW									
OS	Synthetic.								
XX									
FH	Key	Location/Qualifiers							
FT	modified_base	1..27							
FT		/*tag=	a						
FT		/mod_base=	"OTHER"						
FT		/note=	"2'-O-methyl nucleotides"						
XX	PN	WO200166721-A2.							
XX	PD	13-SEP-2001.							
XX	PR	06-MAR-2001; 2001WO-US07163.							
XX	PR	05-MAR-2000; 2000US0-187128P.							
PA	(RIBO-) RIBOZYME PHARM INC.								
XX	PI	Uzman N, McSwiggen JA, Zilnien S, Selwert S, Haeberli P; Chowrira B, Blatt L; WPT; 2001-616242/71.							
PT	New nucleic acid sensor molecule useful in diagnostic applications, nucleic acid-based electronics and functional genomics, comprises an								

PS XX enzymatic nucleic acid and one or more sensors -
 CC XX Example 1; Page 69; 115pp; English.
 CC CC The invention relates to a nucleic acid sensor molecule (1) comprising an
 CC CC enzymatic nucleic acid component and one or more sensor components. (1)
 CC CC is useful in diagnostic applications to identify the presence of genes
 CC CC and/or gene products indicative of a particular genotype and/or
 CC CC phenotype, e.g., a disease state or infection and for diagnosis of disease
 CC CC states or physiological abnormalities related to the expression of viral,
 CC CC bacterial or cellular RNA and DNA. (1) is useful in nucleic acid-based
 CC CC electronics, for the detection of specific target signalling molecules,
 CC CC in assays to assess the specificity, toxicity and effectiveness of
 CC CC various small molecules, nucleoside analogues or non-nucleic acid drugs
 CC CC or for detection of pathogens, biochemicals, organic or inorganic
 CC CC compounds. The present sequence is that of a nucleic acid sensor molecule
 CC CC of the invention.
 XX SQ Sequence 27 BP; 8 A; 10 C; 5 G; 4 U; 0 other;
 Query Match 100.0%; Score 24; DB 22; Length 27;
 Best Local Similarity 83.3%; pred. No. 4.e-05;
 Matches 20; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ctgcgaagcaccatatacgaggat 24
 Db 3 cucgcaagcaccuauacagcagu 26
 RESULT 22
 ABA02738/c
 ID ABA02738 standard; RNA; 27 BP.
 XX AC ABA02738;
 XX DT 12-FEB-2002 (first entry)
 DE Nucleic acid sensor molecule SEQ ID NO 10.
 XX Nucleic acid sensor molecule; detection; infection; disease diagnosis;
 KW physiological abnormality; electronic; signalling molecule;
 KW nucleoside analogue; ss;
 OS Synthetic.
 XX PN WO200166721-A2.
 XX PD 13-SEP-2001.
 XX PF 06-MAR-2001; 2001WO-US07163.
 XX PR 06-MAR-2000; 2000US-18718P.
 PA (RIBO-) RIBOZYME PHARM INC.
 XX Usman N; McSwiggen JA; Zinnen S; Seiwert S; Haeberli P;
 PI Chowrira B; Blatt L;
 XX DR WPI; 2001-616242/71.
 XX PT New nucleic acid sensor molecule useful in diagnostic applications,
 PT nucleic acid-based electronics and functional genomics, comprises an
 PT enzymatic nucleic acid and one or more sensors -
 XX PS Example 1; Page 69; 115pp; English.
 XX The invention relates to a nucleic acid sensor molecule (1) comprising an
 CC enzymatic nucleic acid component and one or more sensor components. (1)
 CC is useful in diagnostic applications to identify the presence of genes
 CC and/or gene products indicative of a particular genotype and/or
 CC phenotype, e.g., a disease state or infection and for diagnosis of disease
 CC states or physiological abnormalities related to the expression of viral,
 CC

CC bacterial or cellular RNA and DNA. (I) is useful in nucleic acid-based electronics, for the detection of specific target signalling molecules, CC in assays to assess the specificity, toxicity and effectiveness of various small molecules, nucleoside analogues or non-nucleic acid drugs CC or for detection of pathogens, biochemicals, organic or inorganic compounds. The present sequence is that of a nucleic acid sensor molecule CC of the invention.

CC Sequence 27 BP; 4 A; 5 C; 10 G; 8 U; 0 other;

CC Query Match 100.0%; Score 24; DB 22; Length 27;

CC Best Local Similarity 100.0%; Pred. No. 4.4e-05; Mismatches 0;

CC Matches 24; Conservative 0; Indels 0; Gaps 0;

CC SQ

CC RESULT 23

CC AAH78439

CC ID AAH78439 standard; DNA; 27 BP.

CC XX

CC AC AAH78439;

CC DT 10-DEC-2001 (first entry)

CC XX

CC DE PCR primer used to amplify HCV cDNA fragment.

CC XX

CC KW Protein isolation; magnetic colloidal particle; polymer envelope;

CC KW vaccine; HCV; PCR primer; ss.

CC OS Hepatitis C virus.

CC XX

CC PN WO200152612-A2.

CC XX

CC PD 26-JUL-2001.

CC XX

CC PF 22-JAN-2001; 2001WO-FR00205.

CC XX

CC PR 21-JAN-2000; 2000FR-0000062.

CC XX

CC PA (INMR) BIO MERIEUX.

CC XX

CC PI Elaiszari A, Mandrand B, Delair T, Spencer D, Arkis A;

CC XX

CC PR WPI; 2001-596423/67.

CC XX

CC PT Isolation of protein and protein-nucleic acid complexes, useful e.g. for subsequent analysis or transport, by binding to magnetic beads

CC XX

CC PS Coated with functionalized polymer

CC XX

CC Example 4; Page 13; 29pp; French.

CC XX

CC The specification describes a method for the isolation of proteins and/or their complexes with nucleic acid. The method comprises treating

CC a sample with magnetic colloidal particles that comprise a magnetic core and an envelope of a polymer (P1) containing ionizable functional groups. The mixture is incubated then the proteins or complexes are recovered by application of a magnetic field. The core is covered by at least one polymer (P2) containing functional groups, at least some of which have reacted with groups in (P1). Functional groups in P1 and P2 are the same or different, and are amino, hydroxy thiol, formyl, ester, anhydride, acyl chloride, carbamate, carbamate and/or iso(thio)cyanate. The method is used for extraction, identification, detection and/or quantification of protein and their complexes. It is also used for establishing cell cultures and biological samples. The complexes formed between magnetic colloidal particles and the proteins are useful for transfer, transport and/or storage of infectious agents (virus, bacterium or yeast) and for preparation of vaccines. PCR primers AAH78440-41 were used to amplify a fragment of HCV cDNA. The amplified fragment was used to demonstrate the use of the method of the invention for capture of HCV particles by magnetic latex.

CC SQ Sequence 27 BP; 8 A; 10 C; 5 G; 4 T; 0 other;

CC Query Match 100.0%; Score 24; DB 22; Length 27;

CC Best Local Similarity 100.0%; Pred. No. 4.4e-05; Mismatches 0;

CC Matches 24; Conservative 0; Indels 0; Gaps 0;

CC SQ

CC RESULT 24

CC AAH78441

CC ID AAH78441 standard; DNA; 27 BP.

CC XX

CC AC AAH78441;

CC DT 10-DEC-2001 (first entry)

CC XX

CC DE PCR primer used to amplify HCV cDNA fragment.

CC XX

CC KW Protein isolation; magnetic colloidal particle; polymer envelope;

CC KW vaccine; HCV; PCR primer; ss.

CC OS Hepatitis C virus.

CC XX

CC PN WO200152612-A2.

CC XX

CC PD 26-JUL-2001.

CC XX

CC PF 22-JAN-2001; 2001WO-FR00205.

CC XX

CC PR 21-JAN-2000; 2000FR-0000062.

CC XX

CC PA (INMR) BIO MERIEUX.

CC XX

CC PI Elaiszari A, Mandrand B, Delair T, Spencer D, Arkis A;

CC XX

CC PR WPI; 2001-596423/67.

CC XX

CC PT Isolation of protein and protein-nucleic acid complexes, useful e.g. for subsequent analysis or transport, by binding to magnetic beads

CC XX

CC PS Coated with functionalized polymer

CC XX

CC Example 4; Page 13; 29pp; French.

CC XX

CC The specification describes a method for the isolation of proteins and/or their complexes with nucleic acid. The method comprises treating

CC a sample with magnetic colloidal particles that comprise a magnetic core and an envelope of a polymer (P1) containing ionizable functional groups. The mixture is incubated then the proteins or complexes are recovered by application of a magnetic field. The core is covered by at least one polymer (P2) containing functional groups, at least some of which have reacted with groups in (P1). Functional groups in P1 and P2 are the same or different, and are amino, hydroxy thiol, formyl, ester, anhydride, acyl chloride, carbamate, carbamate and/or iso(thio)cyanate. The method is used for extraction, identification, detection and/or quantification of protein and their complexes. It is also used for establishing cell cultures and biological samples. The complexes formed between magnetic colloidal particles and the proteins are useful for transfer, transport and/or storage of infectious agents (virus, bacterium or yeast) and for preparation of vaccines. PCR primers AAH78440-41 were used to amplify a fragment of HCV cDNA. The amplified fragment was used to demonstrate the use of the method of the invention for capture of HCV particles by magnetic latex.

CC SQ Sequence 27 BP; 8 A; 10 C; 5 G; 4 T; 0 other;

CC Query Match 100.0%; Score 24; DB 22; Length 27;

CC Best Local Similarity 100.0%; Pred. No. 4.4e-05; Mismatches 0;

CC Matches 24; Conservative 0; Indels 0; Gaps 0;

CC SQ

CC RESULT 25

CC AAH78440-39

CC ID AAH78440-39 standard; DNA; 27 BP.

CC XX

CC AC AAH78440-39;

CC DT 10-DEC-2001 (first entry)

CC XX

CC DE PCR primer used to amplify HCV cDNA fragment.

CC XX

CC KW Protein isolation; magnetic colloidal particle; polymer envelope;

CC KW vaccine; HCV; PCR primer; ss.

CC OS Hepatitis C virus.

CC XX

CC PN WO200152612-A2.

CC XX

CC PD 26-JUL-2001.

CC XX

CC PF 22-JAN-2001; 2001WO-FR00205.

CC XX

CC PR 21-JAN-2000; 2000FR-0000062.

CC XX

CC PA (INMR) BIO MERIEUX.

CC XX

CC PI Elaiszari A, Mandrand B, Delair T, Spencer D, Arkis A;

CC XX

CC PR WPI; 2001-596423/67.

CC XX

CC PT Isolation of protein and protein-nucleic acid complexes, useful e.g. for subsequent analysis or transport, by binding to magnetic beads

CC XX

CC PS Coated with functionalized polymer

CC XX

CC Example 4; Page 13; 29pp; French.

CC XX

CC The specification describes a method for the isolation of proteins and/or their complexes with nucleic acid. The method comprises treating

CC a sample with magnetic colloidal particles that comprise a magnetic core and an envelope of a polymer (P1) containing ionizable functional groups. The mixture is incubated then the proteins or complexes are recovered by application of a magnetic field. The core is covered by at least one polymer (P2) containing functional groups, at least some of which have reacted with groups in (P1). Functional groups in P1 and P2 are the same or different, and are amino, hydroxy thiol, formyl, ester, anhydride, acyl chloride, carbamate, carbamate and/or iso(thio)cyanate. The method is used for extraction, identification, detection and/or quantification of protein and their complexes. It is also used for establishing cell cultures and biological samples. The complexes formed between magnetic colloidal particles and the proteins are useful for transfer, transport and/or storage of infectious agents (virus, bacterium or yeast) and for preparation of vaccines. PCR primers AAH78440-41 were used to amplify a fragment of HCV cDNA. The amplified fragment was used to demonstrate the use of the method of the invention for capture of HCV particles by magnetic latex.

CC SQ Sequence 27 BP; 8 A; 10 C; 5 G; 4 T; 0 other;

CC Query Match 100.0%; Score 24; DB 22; Length 27;

CC Best Local Similarity 100.0%; Pred. No. 4.4e-05; Mismatches 0;

CC Matches 24; Conservative 0; Indels 0; Gaps 0;

CC SQ

CC RESULT 26

CC AAH78440-41

CC ID AAH78440-41 standard; DNA; 27 BP.

CC XX

CC AC AAH78440-41;

CC DT 10-DEC-2001 (first entry)

CC XX

CC DE PCR primer used to amplify HCV cDNA fragment.

CC XX

CC KW Protein isolation; magnetic colloidal particle; polymer envelope;

CC KW vaccine; HCV; PCR primer; ss.

CC OS Hepatitis C virus.

CC XX

CC PN WO200152612-A2.

CC XX

CC PD 26-JUL-2001.

CC XX

CC PF 22-JAN-2001; 2001WO-FR00205.

CC XX

CC PR 21-JAN-2000; 2000FR-0000062.

CC XX

CC PA (INMR) BIO MERIEUX.

CC XX

CC PI Elaiszari A, Mandrand B, Delair T, Spencer D, Arkis A;

CC XX

CC PR WPI; 2001-596423/67.

CC XX

CC PT Isolation of protein and protein-nucleic acid complexes, useful e.g. for subsequent analysis or transport, by binding to magnetic beads

CC XX

CC PS Coated with functionalized polymer

CC XX

CC Example 4; Page 13; 29pp; French.

CC XX

CC The specification describes a method for the isolation of proteins and/or their complexes with nucleic acid. The method comprises treating

CC a sample with magnetic colloidal particles that comprise a magnetic core and an envelope of a polymer (P1) containing ionizable functional groups. The mixture is incubated then the proteins or complexes are recovered by application of a magnetic field. The core is covered by at least one polymer (P2) containing functional groups, at least some of which have reacted with groups in (P1). Functional groups in P1 and P2 are the same or different, and are amino, hydroxy thiol, formyl, ester, anhydride, acyl chloride, carbamate, carbamate and/or iso(thio)cyanate. The method is used for extraction, identification, detection and/or quantification of protein and their complexes. It is also used for establishing cell cultures and biological samples. The complexes formed between magnetic colloidal particles and the proteins are useful for transfer, transport and/or storage of infectious agents (virus, bacterium or yeast) and for preparation of vaccines. PCR primers AAH78440-41 were used to amplify a fragment of HCV cDNA. The amplified fragment was used to demonstrate the use of the method of the invention for capture of HCV particles by magnetic latex.

CC SQ Sequence 27 BP; 8 A; 10 C; 5 G; 4 T; 0 other;

CC Query Match 100.0%; Score 24; DB 22; Length 27;

CC Best Local Similarity 100.0%; Pred. No. 4.4e-05; Mismatches 0;

CC Matches 24; Conservative 0; Indels 0; Gaps 0;

CC SQ

CC RESULT 27

CC AAH78440-41

CC ID AAH78440-41 standard; DNA; 27 BP.

CC XX

CC AC AAH78440-41;

CC DT 10-DEC-2001 (first entry)

CC XX

CC DE PCR primer used to amplify HCV cDNA fragment.

CC XX

CC KW Protein isolation; magnetic colloidal particle; polymer envelope;

CC KW vaccine; HCV; PCR primer; ss.

CC OS Hepatitis C virus.

CC XX

CC PN WO200152612-A2.

CC XX

CC PD 26-JUL-2001.

CC XX

CC PF 22-JAN-2001; 2001WO-FR00205.

CC XX

CC PR 21-JAN-2000; 2000FR-0000062.

CC XX

CC PA (INMR) BIO MERIEUX.

CC XX

CC PI Elaiszari A, Mandrand B, Delair T, Spencer D, Arkis A;

CC XX

CC PR WPI; 2001-596423/67.

CC XX

CC PT Isolation of protein and protein-nucleic acid complexes, useful e.g. for subsequent analysis or transport, by binding to magnetic beads

CC XX

CC PS Coated with functionalized polymer

CC XX

CC Example 4; Page 13; 29pp; French.

CC XX

CC The specification describes a method for the isolation of proteins and/or their complexes with nucleic acid. The method comprises treating

CC a sample with magnetic colloidal particles that comprise a magnetic core and an envelope of a polymer (P1) containing ionizable functional groups. The mixture is incubated then the proteins or complexes are recovered by application of a magnetic field. The core is covered by at least one polymer (P2) containing functional groups, at least some of which have reacted with groups in (P1). Functional groups in P1 and P2 are the same or different, and are amino, hydroxy thiol, formyl, ester, anhydride, acyl chloride, carbamate, carbamate and/or iso(thio)cyanate. The method is used for extraction, identification, detection and/or quantification of protein and their complexes. It is also used for establishing cell cultures and biological samples. The complexes formed between magnetic colloidal particles and the proteins are useful for transfer, transport and/or storage of infectious agents (virus, bacterium or yeast) and for preparation of vaccines. PCR primers AAH78440-41 were used to amplify a fragment of HCV cDNA. The amplified fragment was used to demonstrate the use of the method of the invention for capture of HCV particles by magnetic latex.

CC SQ Sequence 27 BP; 8 A; 10 C; 5 G; 4 T; 0 other;

CC Query Match 100.0%; Score 24; DB 22; Length 27;

CC Best Local Similarity 100.0%; Pred. No. 4.4e-05; Mismatches 0;

CC Matches 24; Conservative 0; Indels 0; Gaps 0;

CC SQ

XX	PI	Blatt L,	McSwiggen J,	Chowrira B M.
XX	XX			
DR	WPI;	2001-607195/69.		
XX	PT	Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense constructs, which down regulate expression of a CD20 gene or neurite growth inhibitor gene useful for treating, e.g., lymphoma, leukemia, and central nervous system injury		
XX	PT	The nucleic acids may be enzymatic nucleic acids (e.g. a ribozyme or a DNazyme), an enzyme, an endolytic nucleic acid cleaving an RNA molecule possessing an NCH motif), a G-cleaver (cleaving RNA with a NN motif) or an ambezyme (cleaving RNA with an NGN triplet), a zinzyme to cleave RNA of CD20 in the presence of a divalent cation that is preferably Mg ²⁺ . Furthermore, it may be contacted with a cell to reduce CD20 activity of the cell and treat a patient having a condition associated with the level of CD20. The treatment may further comprise the use of one or more therapies. In particular, the CD20 targetting nucleic acid may be used to treat lymphoma, leukaemia, B-cell lymphoma, low-grade or follicular non-Hodgkin's lymphoma (NHL), bulky immunodeficiency virus) associated NHL, mantle-cell lymphoma (MCL), immunocytoma (IMC), small B-cell lymphocytic lymphoma, immune thrombocytopenia, and inflammatory arthropathy. The NOGO-targetting nucleic acid is used to cleave RNA of the NOGO gene in the presence of a divalent cation that is preferably Mg ²⁺ . Furthermore, the nucleic acid may be contacted with a cell to reduce NOGO activity of the cell and treat a patient having a condition associated with the level of NOGO. The treatment may further comprise the use of one or more therapies. In particular, the NOGO-targetting nucleic acid may be used to treat central nervous system (CNS) injury and cerebrovascular accident (CVA, stroke), Alzheimer's disease, dementia, multiple sclerosis (MS), chemotherapy induced neuropathy, amyotrophic lateral sclerosis (ALS), Parkinson's disease, ataxia, Huntington's disease, Creutzfeldt-Jakob disease, muscular dystrophy, and/or other neurodegenerative disease states which respond to the modulation of NOGO expression. The present sequence is an enzymatic nucleic acid with trans-acting inhibitory sequences (S'-are substrate sequences, Rz- are enzymatic nucleic acid and I- are inhibitory sequences).		
XX	PS	Example 7; Page 170; 200pp; English.		
CC	CC	The invention relates to a nucleic acid molecule which down regulates expression of a CD20 gene and a nucleic acid molecule which down regulates expression of a neurite growth inhibitor gene (NOGO).		
CC	CC	The nucleic acids may be enzymatic nucleic acids (e.g. a ribozyme or a DNazyme), an enzyme, an endolytic nucleic acid cleaving an RNA molecule possessing an NCH motif), a G-cleaver (cleaving RNA with a NN motif) or an ambezyme (cleaving RNA with an NGN triplet), a zinzyme to cleave RNA of CD20 in the presence of a divalent cation that is preferably Mg ²⁺ . Furthermore, it may be contacted with a cell to reduce CD20 activity of the cell and treat a patient having a condition associated with the level of CD20. The treatment may further comprise the use of one or more therapies. In particular, the CD20 targetting nucleic acid may be used to treat lymphoma, leukaemia, B-cell lymphoma, low-grade or follicular non-Hodgkin's lymphoma (NHL), bulky immunodeficiency virus) associated NHL, mantle-cell lymphoma (MCL), immunocytoma (IMC), small B-cell lymphocytic lymphoma, immune thrombocytopenia, and inflammatory arthropathy. The NOGO-targetting nucleic acid is used to cleave RNA of the NOGO gene in the presence of a divalent cation that is preferably Mg ²⁺ . Furthermore, the nucleic acid may be contacted with a cell to reduce NOGO activity of the cell and treat a patient having a condition associated with the level of NOGO. The treatment may further comprise the use of one or more therapies. In particular, the NOGO-targetting nucleic acid may be used to treat central nervous system (CNS) injury and cerebrovascular accident (CVA, stroke), Alzheimer's disease, dementia, multiple sclerosis (MS), chemotherapy induced neuropathy, amyotrophic lateral sclerosis (ALS), Parkinson's disease, ataxia, Huntington's disease, Creutzfeldt-Jakob disease, muscular dystrophy, and/or other neurodegenerative disease states which respond to the modulation of NOGO expression. The present sequence is an enzymatic nucleic acid with trans-acting inhibitory sequences (S'-are substrate sequences, Rz- are enzymatic nucleic acid and I- are inhibitory sequences).		
CC	SQ	Sequence 27 BP; 4 A; 5 C; 10 G; 8 U; 0 other;		
Query Match	100.0%	Score 24; DB 23; Length 27;		
Best Local Similarity	100.0%	Pred. No. 4 4e-05;		
Matches	24;	Conservative 0; Mismatches 0;		
Indels	0;	Gaps 0;		
Oy	1	ctcgcaagcacctatcaggagt 24		
Db	2	ctcgcaagcacctatcaggagt 25		
RESULT	28			
ID	AZ25757	standard; DNA; 28 BP.		
XX	XX			
AC	AAZ25757;			
XX	XX			
DT	05-APR-2000	(first entry)		
XX	XX			
DE	Hepatitis C virus antisense inhibitor oligonucleotide A312.			
XX	XX			
KW	Hepatitis C virus; HCV; antisense oligonucleotide; hepatotropic; ss; anti-inflammatory; translation inhibition; HCV infection; virucide.			
OS	Hepatitis C virus.			
XX	XX			
PN	US6001990-A.			
XX	XX			
PD	14-DEC-1999.			
XX	XX			
PF	07-JUN-1995;	95US-0474700.		
XX	XX			
PR	10-MAY-1994;	94US-0240382.		
XX	XX			
PA	(GEHO) GEN HOSPITAL CORP.			
XX	XX			
PI	Moradpour D,	Wands JR,	Wakita T;	
XX	XX			

DR WPI; 2000-104900/09.
 XX
 PT Antisense oligonucleotide to Hepatitis C virus RNA, useful for treating
 Hepatitis C virus infections
 XX
 PS Claim 1; Column 23; 31pp; English.

This sequence is an antisense oligonucleotide that hybridises to Hepatitis C virus (HCV) RNA, under physiological conditions. The invention relates to HCV antisense oligonucleotides, and also for a vector comprising a nucleotide sequence which is transcribed in an animal cell to generate an antisense oligonucleotide. The oligonucleotides have virucide, hepatotropic and anti-inflammatory activity, and are useful for treating HCV infection by inhibiting translation of type I-V HCV RNA. Hepatitis C virus is a positive strand RNA virus, and is the major causative agent of post-transfusion hepatitis. Persistent HCV infection can lead to chronic hepatitis, cirrhosis, and hepatocellular carcinoma.

XX Sequence 28 BP; 8 A; 11 C; 5 G; 4 T; 0 other;

Query Match 100.0%; Score 24; DB 21; Length 28;
 Best Local Similarity 100.0%; Pred. No. 4.4e-05; Mismatches 0; Indels 0; Gaps 0;
 Matches 24; Conservative 0; OS Synthetic.

Oy 1 ctgcgaagccctatcaggagt 24
 Db 2 ctgcgaagccctatcaggagt 25

RESULT 29
 AAQ55728
 ID AAQ55728 standard; DNA; 30 BP.
 XX
 AC AAQ55728;
 XX
 DT 13-OCT-1994 (first entry)
 DE Hepatitis C detection primer 2.
 KW Key.
 XX
 OS Synthetic.
 PN JP06014800-A.
 PD 25-JAN-1994.
 PF 02-JUL-1992; 92JP-0197407.
 PR 02-JUL-1992; 92JP-0197407.
 PA (TOYU) TOSOH CORP.
 DR WPI; 1994-061488/08.

XX Detection of human hepatitis C virus - using primer contg. at least 15 continuous bases
 XX
 PS Claim 1; Page 1; 5pp; Japanese.

The primers (AAQ55727-728) are used to detect hepatitis C virus. The method can amplify and detect specifically the nucleic acid sequence originated from a trace amount of HCV contained in a sample.

XX Sequence 30 BP; 8 A; 12 C; 6 G; 4 T; 0 other;

Query Match 100.0%; Score 24; DB 13; Length 33;
 Best Local Similarity 100.0%; Pred. No. 4.4e-05; Mismatches 0; Indels 0; Gaps 0;
 Matches 24; Conservative 0; OS Synthetic.

Oy 1 ctgcgaagccctatcaggagt 24
 Db 7 ctgcgaagccctatcaggagt 30

RESULT 31
 AAQ46464
 ID AAQ46464 standard; DNA; 33 BP.
 XX
 AC AAQ46464;
 XX
 DT 13-DEC-1993 (first entry)
 DE Hepatitis C virus RNA assay capture probe HCV.33.9.
 XX
 KW Detection; HCV; reduced background signal; improved reproducibility; hybridisation; 5'-untranslated region; C gene; ss.
 XX
 OS Synthetic.

Query Match 100.0%; Score 24; DB 15; Length 30;
 Best Local Similarity 100.0%; Pred. No. 4.4e-05; Mismatches 0; Indels 0; Gaps 0;
 Matches 24; Conservative 0; OS Synthetic.

Oy	1	ctcgcaagcacctatcaggcagt	24		100.0%; Score 24; DB 19; Length 40;	Best Local Similarity 100.0%; Pred. No. 4.4e-05; Mismatches 0; Indels 0; Gaps 0;
Db	13	ctcgcaagcacccatcaggcagt	36		100.0%; Score 36; DB 19; Length 40;	Best Local Similarity 100.0%; Pred. No. 4.4e-05; Mismatches 0; Indels 0; Gaps 0;
RESULT	35					
	AAQ98139	standard; DNA; 53 BP.				
ID	AAQ98139					
XX	AAQ98139;					
XX						
DT	05-FEB-1996	(first entry)				
XX						
DE	Control label extender probe used in an HCV sandwich hybridisation assay.					
XX						
KW	Probe; nucleotide; solution phase sandwich hybridisation assay;					
KW	competitive; analyte binding sequence; background signal reduction;					
KW	comb body; Hepatitis C virus; ss.					
XX						
OS	Synthetic.					
XX						
Key	Location/Qualifiers					
XX	21..53					
FT	/tag= ^a "hybridises to target sequence"					
FT	/note= "hybridises to target sequence"					
XX						
PN	WO9516055-A1.					
XX						
PD	15-JUN-1995.					
XX						
PF	07-DEC-1994; 94WO-US14119.					
XX						
PR	08-DEC-1993; 93US-0164388.					
XX						
PA	(CHIR) CHIRON CORP.					
XX						
PI	Collins M, Fultz T, Urdea MS, Warner BD;					
XX						
DR	WPI; 1995-224335/29.					
XX						
PT	Soln. phase sandwich hybridisation assays for nucleic acid(s) - with					
PT	capture extender molecules or competitive oligo:nucleotide(s) to					
PT	minimise background signal, increasing sensitivity and selectivity					
XX						
PS	Example 2; Page 43; 86pp; English.					
XX						
CC	AAQ98125-098143 are control label extender probes (LEPs) used in a					
CC	hepatitis C virus sandwich hybridisation assay used to demonstrate a					
CC	variation of a new improved method of a solution phase sandwich					
CC	hybridisation assay in which LEPs are used with a capture probe (CP).					
CC	One label extender probe binds the target DNA and another binds to a					
CC	labelledprobe(LP).					
CC	The new method minimises background signals (caused by non-specific					
CC	hybridisation), this improves both sensitivity and selectivity of					
CC	the assay without increasing cost or time.					
XX						
SQ	Sequence 53 BP; 12 A; 17 C; 15 G; 9 T; 0 other;					
Query	Match	100.0%; Score 24; DB 16; Length 53;				
Best Local	Similarity	100.0%; Pred. No. 4.4e-05;				
Matches	24;	Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
Oy	1	ctcgcaagcacctatcaggcagt	24		100.0%; Score 24; DB 19; Length 40;	Best Local Similarity 100.0%; Pred. No. 4.4e-05; Mismatches 0; Indels 0; Gaps 0;
Db	27	ctcgcaagcacccatcaggcagt	50		100.0%; Score 50; DB 19; Length 40;	Best Local Similarity 100.0%; Pred. No. 4.4e-05; Mismatches 0; Indels 0; Gaps 0;

RESULT 36
 AAQ98104 PD 09-DEC-1993.
 ID AAQ98104 standard; DNA; 53 BP.
 XX XX
 AC AC AAQ98104;
 XX XX
 DT 05-FEB-1996 (first entry)
 DE Label extender probe used in an improved sandwich hybridisation assay.
 XX XX
 KW Probe; nucleotide; solution phase sandwich hybridisation assay;
 SS competitive; analyte binding sequence; background signal reduction;
 OS Synthetic.
 XX XX
 PN WO9516055-A1.
 XX XX
 PD 15-JUN-1995.
 XX XX
 PP 07-DEC-1994; 94WO-US14119.
 XX XX
 PR 08-DEC-1993; 93US5-0164388.
 XX XX
 PA (CHIR) CHIRON CORP.
 XX XX
 PI Collins M, Fultz T, Urdea MS, Warner BD;
 DR DR
 XX XX
 PT Soln. phase sandwich hybridisation assays for nucleic acids(s) - with
 PT capture extender molecules or competitive oligo;nucleotide(s) to
 PT minimise background signal, increasing sensitivity and selectivity
 XX XX
 PS Example 1: Page 33; 86pp; English.

AAQ98100-098105 are label extender probes (LEPs) used in a variation
 CC of a new improved method of a solution phase sandwich hybridisation
 assay in which LEPs are used with a capture probe (CP). One label
 CC extender probe binds the target DNA and another binds to a labelled
 CC probe (LP).
 CC The new method minimises background signals (caused by non-specific
 CC hybridisation), thus improves both sensitivity and selectivity of
 CC the assay without increasing cost or time.
 XX Sequence 53 BP; 12 A; 17 C; 15 G; 9 T; 0 other;

Query Match 100 %; Score 24; DB 14; Length 57;
 CC Best Local Similarity 100 %; Pred. No. 4.4e-05;
 CC Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 CC QY 1 ctgcgaagccatcatcagaagt 24
 CC Db 57 CTGCAGACCCATCAGGAGT 34

RESULT 38
 AAZ23543/C ID AAZ23543 standard; DNA; 59 BP.
 XX XX
 AC AC AAZ23543;
 XX XX
 DT 21-DEC-1999 (first entry)
 DE HCV DNA fragment 2.
 XX XX
 KW Assay; amplification; hybridisation; probe; detection; viral; bacterial;
 KW cellular; yeast; fungal; primer; ss.
 XX XX
 OS Hepatitis C virus.
 PN PN DE19814828-A1.
 XX XX
 PD 07-OCT-1999.
 XX XX
 PR 02-APR-1998; 98DE-101428.
 XX XX
 PR 02-APR-1998; 98DE-101428.
 XX XX
 PA (HOF) ROCHE DIAGNOSTICS GMBH.
 XX XX
 PI Kessler C, Haberhausen G, Batz H, Oerum H;
 XX DR DR
 XX XX
 DE Hepatitis C virus probe target region.
 XX XX
 KW Detection; HCV; 11:2 probe design.
 XX XX
 OS Hepatitis C virus.
 XX XX
 PN WO9324656-A.

RESULT 37
 AAQ62223/C ID AAQ62223 standard; RNA; 57 BP.
 XX XX
 AC AC AAQ62223;
 XX XX
 DT 13-JUN-1994 (first entry)
 XX XX
 DE Hepatitis C virus probe target region.
 XX XX
 KW Detection; HCV; 11:2 probe design.
 XX XX
 OS Hepatitis C virus.
 XX XX
 PN WO9324656-A.

This invention describes a novel assay for a nucleic acid comprises:
 CC (a) generating amplification products from a fragment of the nucleic

acid, (b) contacting the amplification products with a probe; and (c) detecting hybridization between the amplification product and the probe. The assay is useful for detection of viral, bacterial, cellular, yeast or fungal nucleic acids in human, animal, bacterial, plant, yeast or tissue samples, e.g., feces, smears, cell suspensions, cultures or fragment of the HCV genome used in the method of the invention.

CC
CC
CC
CC
CC
CC
CC
XX
SQ Sequence 59 BP; 9 A; 16 C; 21 G; 13 T; 0 other;
Query Match 100.0%; Score 24; DB 20; Length 59;
Best Local Similarity 100.0%; Pred. No. 4.4e-05;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ctgcgaagccctatcaggagt 24
Db 26 CTGGAGACCTATCAGGAGT 3

RESULT 39
AAZ09795/c
ID AAZ09795 standard; DNA; 59 BP.
XX
AC AAZ09795;
XX
DT 26-NOV-1999 (first entry)
DE HCV DNA probe.
XX
KW Probe; amplification; primer; reporter group; quencher group; PCR; amplicon; detection; ss.
XX
OS Synthetic.
OS Hepatitis C virus.
XX
PN DE19814001-A1.
XX
PD 30-SEP-1999.
XX
PP 28-MAR-1998; 98DE-1014001.
XX
PR 28-MAR-1998; 98DE-1014001.
PA (HOFF) ROCHE DIAGNOSTICS GMBH.
XX
PI Kessler C, Haberhausen G, Batz H, Orum H;
XX
DR WPI; 1999 552213/47.
XX
PT Fluorescent nucleic acid amplification assay, useful for detection of viral, bacterial, cellular, yeast or fungal nucleic acids
XX
PS Disclosure; Fig 4; 16pp; German.
XX
This invention describes a novel assay for a nucleic acid which comprises an amplification reaction using two non-overlapping primers, polymerase with 5'-nuclease activity and a probe with reporter groups and quencher groups that binds a region other than that bound by the primers. The reaction generates products of less than 100 nucleotides. The assay is useful for detection of viral, bacterial, cellular, yeast or fungal nucleic acids in human, animal, plant, yeast or fungal samples, e.g. feces, smears, cell suspensions, cultures or tissue, cell or liquid biopsy samples. Compared with assays in which longer amplification products are generated, the assay can be performed more rapidly using shorter polymerase chain reaction (PCR) cycles, sensitivity may be increased due to reduced competition between the short counterstrand of the amplicon and the detector probe. Specificity may also be increased because of the increased relative length of sequence B compared with the total length of the amplicon and the differentiability of subtypes may be increased. In addition signal-to-noise ratios may be increased with the new method because short amplicons have reduced potential for nonspecific hybridization. In addition reproducibility may

CC be increased because small target regions on RNA genomes are less sensitive to RNA degradation, and the possibilities for secondary structure formation are reduced. This sequence represents a probe used to detect hepatitis C virus which is used to illustrate the method of the invention.

CC Query Match 100.0%; Score 24; DB 20; Length 59;
Best Local Similarity 100.0%; Pred. No. 4.4e-05;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ctgcgaagccctatcaggagt 24
Db 26 CTGGAAAGCACCTATCAGGAGT 3

RESULT 40
AAQ98121
ID AAQ98121 standard; DNA; 64 BP.
XX
AC AAQ98121;
XX
DT 05-FEB-1996 (first entry)
DE Label extender probe used in an HCV sandwich hybridisation assay.
XX
KW Probe; nucleotide; solution phase sandwich hybridisation assay; competitive; analyte binding sequence; background signal reduction; comb body; Hepatitis C virus; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT misc_binding 17.49
FT /*tgc-^a/note= "hybridises to target sequence"
XX
PN WO9516055-A1.
XX
PD 15-JUN-1995.
XX
PP 07-DBC-1994; 94WO-US14119.
XX
PR 08-DEC-1993; 93US-0164388.
XX
PA (CHIR) CHIRON CORP.
XX
PI Collins M, Fultz T, Urdea MS, Warner BD;
XX
DR WPI; 1995-224335/29.
XX
PT Soln. phase sandwich hybridisation assays for nucleic acid(s) - with capture extender molecules or competitive oligo:nucleotid(e)s) to minimise background signal, increasing sensitivity and selectivity
XX
PS Example 2; Page 42; 86pp; English.
XX
CC AAQ9818-098121 are label extender probes (LEs) used in a hepatitis C virus sandwich hybridisation assay used to demonstrate a variation of a new improved method of a solution phase sandwich hybridisation assay in which LEs are used with a capture probe (CP). One label extender probe binds the target DNA and another binds to a labelled probe (LP).
CC The new method minimises background signals (caused by non-specific hybridisation), this improves both sensitivity and selectivity of the assay without increasing cost or time.
XX
SQ Sequence 64 BP; 18 A; 16 C; 17 G; 13 T; 0 other;

Query Match 100.0%; Score 24; DB 16; Length 64;

PD 06-AUG-1997.
 XX
 PF 19-AUG-1992; 92EP-0065347.
 XX
 PR 21-JUL-1992; 92US-0910844.
 XX
 PR 27-AUG-1991; 91US-0751305.
 XX
 PA (HOFF) HOFFMANN LA ROCHE & CO AG F.
 XX
 PI Resnick RM, Young KKY;
 DR WPI; 1997-387489/36.

XX
 PS Claims 4 and 5; Page 8; 35pp; English.

PT Oligo:nucleotide probes and primers for detecting hepatitis C virus
 PT nucleic acid - from many different strains without loss of
 specificity' allow single step reverse transcription and
 PT amplification

XX
 PS XX
 CC This oligonucleotide KY95 can be used as a probe for detecting
 CC hepatitis C virus (HCV) nucleic acid from a Japanese or US prototype
 CC strain as well as HCV C9 prototype strain. This oligonucleotide can
 CC also be used as a primer for amplifying HCV nucleic acid. The sequence
 CC of this oligonucleotide is contained in a specific region of HCV genomic
 CC nucleic acid. The probe or the primer is preferably labelled. The probe
 CC is used to detect HCV nucleic acid, preferably after this has been
 CC amplified using the new primer in reverse transcription polymerase chain
 reaction (RT-PCR), for both diagnostic and epidemiological applications.
 CC The primer is effective for both reverse transcription and PCR,
 CC eliminating the need to open the reaction tube during the procedure.
 CC Amplification is effective (no need for a second round of PCR with nested
 CC primers) and provides high sensitivity. The probe is directed to
 CC conserved regions and so can detect many different strains without loss
 XX

SQ Sequence 29 BP; 8 A; 8 C; 8 G; 5 T; 0 other;

Query Match 95.8%; Score 23; DB 18; Length 29;
 Best Local Similarity 100.0%; Pred. No. 0.00017; Mismatches 0; Indels 0; Gaps 0;
 Matches 23; Conservative 0; CC

Oy 2 tcggaaagccctatcaggagt 24
 ||||| ||||| ||||| |||||
 Db 7 tcgcaagcacccatcaggcgt 29

RESULT 44
 AAQ53259/CC
 ID AAQ53259 standard; DNA; 22 BP.
 XX
 AC AAQ53259;
 XX
 DT 13-JUN-1994 (first entry)
 DE Hepatitis C virus probe.
 XX
 KW Detection; HCV; 11:2 probe design.
 XX
 OS Synthetic.
 XX
 PH Location/Qualifiers
 FT modified_base 22
 FT /*tag= "fluorescein labelled"
 FT /note= "fluorescein labelled"
 XX
 PN WO9324656-A.
 XX
 PD 09-DEC-1993.
 XX
 PR 24-MAY-1993; 93WO-US04863.
 XX

PR 29-MAY-1992; 92US-0891543.
 XX
 PA (ABBO) ABBOTT LAB.
 XX
 PI Carrino JJ, Marshall RL, Sustachek JC;
 DR WPI; 1993-405844/50.

XX
 PS Example 8; Page 25; 49pp; English.

PT Amplifying known RNA target for use in diagnosis of HIV and HCV
 PT infection - by treating sample RNA with oligo-nucleotide probe,
 PT extending probe by reverse transcription of target, dissociating
 PT probe from target, hybridising 2nd probe with 1st, etc.

XX
 PS XX
 CC The sequence is that of a probe which was used in the detection of
 CC hepatitis C virus (HCV) using a 11:2 probe design. The probe is
 CC specific for a part of the 5' UTR of the HPC10MR sequence between
 CC positions 246-302.

XX
 SQ Sequence 22 BP; 3 A; 4 C; 9 G; 6 T; 0 other;

Query Match 91.7%; Score 22; DB 14; Length 22;
 Best Local Similarity 100.0%; Pred. No. 0.00067; Mismatches 0; Indels 0; Gaps 0;
 Matches 22; Conservative 0; CC

Oy 1 ctcgcgaagccctatcaggca 22
 ||||| ||||| ||||| |||||
 Db 22 CTGGCAAGCACCCTACAGGCA 1

RESULT 45
 AAD25564
 ID AAD25564 standard; DNA; 23 BP.
 XX
 AC AAD25564;
 XX
 DT 26-MAR-2002 (first entry)

XX
 DE HCV RNA 5' UTR amplifying PCR primer #2.

KW Hepatitis C virus; HCV; cytostatic; replication defective gene transfer;
 KW encapsidated RNA virus; gene therapy; cancer therapy; PCR primer; ss.
 KW Hepatitis C virus.
 XX
 OS WO200190302-A2.

PN
 XX
 PD 29-NOV-2001.
 XX
 PR 10-MAY-2001; 2001WO-US15449.

XX
 PR 24-MAY-2000; 2000US-206997P.

XX
 PA (FENG/) FENG Y.
 PA (TANG/) TANG H.
 XX
 PT Feng Y, Tang H;
 XX
 DR WPI; 2002-066766/09.

XX
 PT Producing encapsidated RNA virus by coexpressing RNA virus genomic
 PT sequence linked to bacteriophage promoter, and coding sequence for
 PT bacteriophage polymerase linked to poxvirus promoter in eukaryotic cell
 PT cytoplasm -
 XX
 PS Example 1; Page 30; 49pp; English.

XX
 CC The patient discloses methods to produce RNA viral sequences, recombinant
 CC RNA viruses, mutants of RNA viruses and RNA virus-derived vectors in
 CC cell culture and in vitro using non-viable, replication defective helper
 CC vaccinia recombinants. These methods generate RNA viral genomes and viral

CC particles in cell culture and in vitro independent of their natural
CC replication pathways, bypassing the limitation of any cellular barriers.
CC The invention also relates to a method for producing encapsidated RNA
CC virus comprising coexpressing polypeptide coding sequences capable of
CC forming capsid and packaging RNA viral genomic sequence in eukaryotic
CC cell, a construct comprising RNA viral genomic sequence linked to
CC bacteriophage promoter and transcription terminator and bacteriophage
CC polymerase coding sequence, which is operably compatible with the
CC promoter and is linked to poxvirus promoter. The methods are useful
CC for producing infectious or non-infectious, replication-defective,
CC encapsidated RNA viruses such as hepatitis virus comprising an RNA
CC genome e.g. hepatitis C virus (HCV), immature hepatitis B virus or
CC hepatitis A virus, lentivirus, rhinovirus, influenza virus, LCMV,
CC arenavirus, parainfluenza virus, reovirus, rotavirus, astrovirus,
CC filovirus, or coronavirus. They are preferably useful for producing
CC encapsidated human immunodeficiency virus (HIV)-1, where the HIV-1
CC lacks a Rev-response element (RRE) or an envelope sequence. Methods
CC of the invention are also useful for producing replication defective
CC gene transfer and gene therapy vectors, particularly to transfer nucleic
CC acids to human cells in vivo and in vitro. The methods can be used for
CC packaging therapeutic sequences as gene therapy vector preparations that
CC are substantially free of helper virus and used as pharmaceuticals in
CC e.g. gene replacement therapy, or cancer therapy. The present DNA
CC sequence is a PCR primer which is used for amplifying the 5' untranslated
CC region (UTR) of HCV RNA.
XX Sequence 23 BP; 7 A; 9 C; 4 G; 3 T; 0 other;
SQ

Query Match 91.7%; Score 22; DB 24; Length 23;
Best Local Similarity 100.0%; Pred. No. 0.00068; Mismatches 0; Indels 0; Gaps 0;
Matches 22; Conservative 0; OY 1 ctcccaaggaccctatcgca 22
Db 2 ctcccaaggaccctatcgca 23

Search completed: August 26, 2002, 22:24:56
Job time: 6235 sec

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CC conserved. These primer/probes can be used to identify different HCV isolates such as US, Japan and C9 (see also AAQ37597-601).
 XX
 SQ Sequence 24 BP; 6 A; 6 C; 8 G; 4 T; 0 other;

Query Match 100.0%; Score 24; DB 14; Length 24;
 Best Local Similarity 100.0%; Pred. No. 7e-05; Mismatches 0; Indels 0; Gaps 0;
 XX
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 gcagaagcgcttagccatggcgt 24
 Db 1 gcagaagcgcttagccatggcgt 24

RESULT 2
 AAQ79964 standard; DNA; 24 BP.
 XX
 ID AAQ79964
 AC AAQ79964;
 XX
 DT 01-AUG-1995 (first entry)
 XX
 DE Primer KY90 for HCV RNA.
 XX
 KW Primer; PCR; polymerase chain reaction; amplification;
 KW RNA detection; reverse transcription; hepatitis C virus; HCV;
 KW ss.
 XX
 OS Synthetic.
 XX
 PN EP632134-A.
 XX
 CC 04-JAN-1995.
 XX
 PR 20-JUN-1994; 94EP-0109468.
 PR 01-JUL-1993; 93US-0086483.
 XX
 PA (HOFF) HOFFMANN LA ROCHE & CO AG F.
 XX
 PI Gelfand DH, Myers TW, Sigma CL;
 XX
 DR WPI; 1997-387489/36.
 XX
 PT Oligo-nucleotide probes and primers for detecting hepatitis C virus
 PT nucleic acid from many different strains without loss of
 PT specificity; allow single step reverse transcription and
 PT amplification

XX
 PS Claims 2 and 5; Page 7; 35pp; English.
 XX
 CC This oligonucleotide KY80 can be used as a probe for detecting
 hepatitis C virus (HCV) nucleic acid from a Japanese or US prototype
 strain. This oligonucleotide can also be used as a primer for amplifying
 HCV nucleic acid. This primer is capable of amplifying HCV C9 prototype
 strains also. The sequence of this oligonucleotide is contained in a
 CC specific region of HCV genomic nucleic acid. The probe or the primer
 CC is preferably labelled. The probe is used to detect HCV nucleic acid,
 CC preferably after this has been amplified using the new primer in reverse
 CC transcription polymerase chain reaction (RT-PCR), for both diagnostic and
 CC epidemiological applications. The primer is effective for both reverse
 CC transcription and PCR, eliminating the need to open the reaction tube
 CC during the procedure. Amplification is effective (no need for a second
 CC round of PCR with nested primers) and provides high sensitivity. The
 CC probe is directed to conserved regions and so can detect many different
 CC strains without loss of specificity.
 XX
 SQ Sequence 24 BP; 6 A; 6 C; 8 G; 4 T; 0 other;

Query Match 100.0%; Score 24; DB 16; Length 24;
 Best Local Similarity 100.0%; Pred. No. 7e-05; Mismatches 0; Indels 0; Gaps 0;
 XX
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 gcagaagcgcttagccatggcgt 24
 Db 1 gcagaagcgcttagccatggcgt 24

RESULT 3
 AAT64887 standard; DNA; 24 BP.
 XX
 AC AAT64887;
 XX
 DT 12-MAR-1998 (first entry)

XX Hepatitis C virus (HCV) oligonucleotide KY80.
 DE
 XX Hepatitis C virus; reverse transcription; probe; PCR primer;
 KW detection; ss.
 XX OS Synthetic.
 KW Hepatitis C virus.
 XX PR 19-AUG-1992; 92EP-0065347.
 PR 21-JUL-1992; 92US-091844.
 PR 27-AUG-1991; 91US-0751305.
 XX PA (HOFF) HOFFMANN LA ROCHE & CO AG F.
 PR Resnick RM, Young KRY;
 XX DR WPI; 1997-387489/36.
 XX PT Oligo-nucleotide probes and primers for detecting hepatitis C virus
 PT nucleic acid from many different strains without loss of
 PT specificity; allow single step reverse transcription and
 PT amplification

XX
 PS Claims 2 and 5; Page 7; 35pp; English.
 XX
 CC This oligonucleotide KY80 can be used as a probe for detecting
 hepatitis C virus (HCV) nucleic acid from a Japanese or US prototype
 strain. This oligonucleotide can also be used as a primer for amplifying
 HCV nucleic acid. This primer is capable of amplifying HCV C9 prototype
 strains also. The sequence of this oligonucleotide is contained in a
 CC specific region of HCV genomic nucleic acid. The probe or the primer
 CC is preferably labelled. The probe is used to detect HCV nucleic acid,
 CC preferably after this has been amplified using the new primer in reverse
 CC transcription polymerase chain reaction (RT-PCR), for both diagnostic and
 CC epidemiological applications. The primer is effective for both reverse
 CC transcription and PCR, eliminating the need to open the reaction tube
 CC during the procedure. Amplification is effective (no need for a second
 CC round of PCR with nested primers) and provides high sensitivity. The
 CC probe is directed to conserved regions and so can detect many different
 CC strains without loss of specificity.
 XX
 SQ Sequence 24 BP; 6 A; 6 C; 8 G; 4 T; 0 other;

Query Match 100.0%; Score 24; DB 18; Length 24;
 Best Local Similarity 100.0%; Pred. No. 7e-05; Mismatches 0; Indels 0; Gaps 0;
 XX
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 gcagaagcgcttagccatggcgt 24
 Db 1 gcagaagcgcttagccatggcgt 24

RESULT 4
 AAT93541 standard; DNA; 24 BP.
 XX
 ID AAT93541
 XX
 AC AAT93541;
 XX
 DT 19-FEB-1998 (first entry)
 DE Sense primer KY80 for amplification of HCV RNA.
 XX
 KW Armoured RNA; bacteriophage MS2; RT-PCR; ribonuclease; recombinant;
 KW Human immunodeficiency virus; HIV; Hepatitis C Virus; HCV; viral RNA;
 KW detection; quantification standard; maturase protein; coat protein;
 KW PCR primer; OS RNA; reverse transcriptase-PCR; ss.

The present sequence is a primer for hepatitis C virus (HCV) DNA, which was used in the preparation of a nucleic acid standard, comprising a nuclease resistant nucleic acid segment encoding a standard nucleic acid, i.e. RNA. The ribonuclease resistant RNA standard, designated armored RNA (RTM) is useful as an internal or external nucleic acid standard in quantitative assays, e.g. PCR or RT-PCR for the presence of a tested nucleic acid in blood samples.

Sequence 24 BP; 6 A; 6 C; 8 G; 4 T; 0 other;

Query Match
Best Local Similarity 100.0%; Score 24; DB 19; Length 24;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gcagaaacgcgtctagccatggcgt 24

DN 1 gcagaaacgcgtctagccatggcgt 24

Db 1 gcagaaacgcgtctagccatggcgt 24

RESULT 8
ID AA223536
AC AAA23536;
XX

RESULT 8
ID AA223536 standard; DNA; 24 BP.
AC AAA23536;
XX

DT 21-DEC-1999 (first entry)
XX
DE HCV wild type genome primer KY80.
XX
KW Assay; amplification; hybridisation; probe; detection; viral; bacterial;
XX
PR cellular; yeast; fungal; primer; ss.
XX
OS Synthetic.
OS Hepatitis C virus.
XX
PN DE19814828-A1.
XX
PD 07-OCT-1999.
XX
PR 02-APR-1998; 98DE-1014828.
XX
PA (HOFF) ROCHE DIAGNOSTICS GMBH.
XX
PT Kessler C, Haberhausen G, Batz H, Oerum H;
XX
DR WPI; 1999-552286/47.
XX
PT Nucleic acid amplification assay for detecting viral, bacterial,
PT cellular, yeast or fungal nucleic acids -
XX
PS Example 1; Page 19; 28pp; German.
XX
CC This invention describes a novel assay for a nucleic acid comprises:
CC (a) generating amplification products from a fragment of the nucleic
CC acid; (b) contacting the amplification products with a probe; and
CC (c) detecting hybridization between the amplification product and the
CC probe. The assay is useful for detection of viral, bacterial, cellular,
CC yeast or fungal nucleic acids in human, animal, bacterial, plant, yeast
CC or fungal samples, e.g., feces, smears, cell suspensions, cultures or
CC tissue, cell or liquid biopsy samples. This sequence represents a
CC primer used in the method of the invention.
XX
SQ Sequence 24 BP; 6 A; 6 C; 8 G; 4 T; 0 other;

Query Match
Best Local Similarity 100.0%; Score 24; DB 20; Length 24;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gcagaaacgcgtctagccatggcgt 24

DN 1 gcagaaacgcgtctagccatggcgt 24

RESULT 9
ID AA209797
AC AA209797;
XX
DT 26-NOV-1999 (first entry)
XX
DE HCV PCR primer KY80.
XX
KW Probe; amplification; primer; reporter group; quencher group; PCR;

Query Match
Best Local Similarity 100.0%; Score 24; DB 19; Length 24;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gcagaaacgcgtctagccatggcgt 24

XX
OS Synthetic.
OS Hepatitis C virus.
XX
PN DE19814001-A1.
XX
PD 30-SEP-1999.
XX
PF 28-MAR-1998; 98DE-1014001.
XX
PR 28-MAR-1998; 98DE-1014001.
XX
PA (HOFF) ROCHE DIAGNOSTICS GMBH.
XX
PI Kessler, C., Haberhausen G., Batz H., Orum H.;
DR WPI; 1999-552213/47.

PT Fluorescent nucleic acid amplification assay, useful for detection of viral, bacterial, cellular, yeast or fungal nucleic acids
XX
PS Example 1; Page 19; 16pp; German.

XX
CC This invention describes a novel assay for a nucleic acid which comprises an amplification reaction using two non-overlapping primers, a polymerase with 5'-nuclease activity and a probe with reporter groups and quencher groups that binds a region other than that bound by the primers. The assay reaction generates products of less than 100 nucleotides. The assay is useful for detection of viral, bacterial, cellular, yeast or fungal nucleic acids in human, animal, bacterial, plant, yeast or fungal samples, e.g. feces, smears, cell suspensions, cultures or tissue, cell or liquid biopsy samples. Compared with assays in which longer amplification products are generated, the assay can be performed more rapidly using shorter polymerase chain reaction (PCR) cycles, sensitivity may be increased due to reduced competition between the short counterstrand of the amplicon and the detector probe. Specificity may also be increased because of the increased relative length of sequence B compared with the total length of the amplicon and the differentiability of subtypes may be increased. In addition signal-to-noise ratios may be increased with the new method because short amplicons have reduced potential for nonspecific hybridization. In addition reproducibility may be increased because small target regions on RNA genomes are less sensitive to RNA degradation, and the possibilities for secondary structure formation are reduced. This sequence represents a PCR primer used in the amplification of a region of HCV which is used to illustrate the method of the invention.

XX
SQ Sequence 24 BP; 6 A; 6 C; 8 G; 4 T; 0 other;

Query	Match	Score	DB	Length
Qy	1 gcaagaagcgttccatcgct 24	100.0%	24	24
Db	1 gcagaaggcttcacccatggct 24			

RESULT 10

ID	RESULT	Score	DB	Length
AAX78451	1	100.0%	24	24
AAX78451 standard; DNA; 24 BP.				

XX
AC AAX78451;
XX
DT 26-AUG-1999 (first entry)

XX
DE HCV PCR primer 1.

XX
ID AAX78451; standard; DNA; 24 BP.

XX
KW RNA standard; HCV; detection; gag gene; cerebrospinal fluid; PCR primer; ribonuclease resistant; encapsulation; viral; HIV-1; HIV-2; HCV; HTLV-1; HTLV-2; hepatitis G; enterovirus; blood-borne pathogen; ss.

XX
PN US5919625-A.
XX
PD 06-JUL-1999.
XX
PF 29-APR-1997; 97US-0841252.
XX
PR 03-JUL-1996; 96US-067553.
XX
PR 29-APR-1997; 97US-0841252.

XX
PA (AMBI-) AMBION INC.
PA (CENE-) CENETRON DIAGNOSTICS LLC.
XX
PI Dubois DB, Pasloske BL, Winkler MM;
XX
DR WPI; 1999-394617/33.

XX
PT Ribonuclease resistant viral RNA standards
XX
PS Example V; Column 31-32; 22pp; English.

XX
CC This invention describes the construction of novel RNA standards for the quantification of human immunodeficiency virus (HIV) and hepatitis C virus (HCV) from e.g. cerebrospinal fluids. The method involves (1) obtaining a sample to be analysed; (2) obtaining a ribonuclease resistant RNA standard, encapsulated in a bacteriophage viral coat protein, which comprises an RNA segment having a segment encoding a sequence that serves as a standard in detection or quantification of the RNA of interest; (3) mixing the sample with the standard; (4) isolating RNA from the mixture, and (5) assaying for the presence of the RNA. The method is useful for the detection or quantification of HIV-1, HIV-2, HCV, HTLV-1, HTLV-2, hepatitis G, an enterovirus, or a blood-borne pathogen. This sequence represents a PCR primer used to amplify a region of the hepatitis C genome which is used in the method of the invention.

XX
SQ Sequence 24 BP; 6 A; 6 C; 8 G; 4 T; 0 other;

Query	Match	Score	DB	Length
Qy	1 gcaagaagcgttccatcgct 24	100.0%	24	24
Db	1 gcagaaggcttcacccatggct 24			

RESULT 11

ID	RESULT	Score	DB	Length
AAX23968	1	100.0%	24	24
AAX23968 standard; DNA; 24 BP.				

XX
AC AAX23968;
XX
DT 28-JUN-1999 (first entry)

XX
DE PCR primer KY80.

XX
KW Amplification; medical; forensic; diagnosis; food analysis; blood; environmental analysis; plant protection; veterinary medicine; human immune deficiency virus; hepatitis B; hepatitis C; Chlamydia; screening; PCR primer; detection; probe; ss.

XX
OS Synthetic.

XX
PN DB19748690-A1.

XX
PD 06-MAY-1999.

XX
PR 04-NOV-1997; 97DE-1048690.

XX
PR 04-NOV-1997; 97DE-1048690.

XX
PA (HOFF) ROCHE DIAGNOSTICS GMBH.
XX
DR WPI; 1999-278780/24.

XX
PT Detecting nucleic acid by generating short amplicons and probing
PT protection
e.g. for diagnosis, food and environmental analysis and plant

XX
PS Example 1; Page 16; 22pp; German.

CC This invention describes a method for the detection of nucleic acid which comprises amplification and reaction of the amplicon with a probe. The method is used to detect nucleic acid e.g. for medical or forensic diagnosis, in food and environmental analysis, in plant protection and veterinary medicine, e.g. for detecting human immune deficiency virus, hepatitis B or C viruses, or Chlamydia, in blood screening. The method provides target-dependent, exponential amplification for highly specific and sensitive, reproducible and quantitative detection of one or more nucleic acids (single or double stranded). The design of primers and probes is sufficiently flexible to allow many nucleic acids to be detected in a standardized reaction format using partly the same primers and probes. Only small amplicons are produced (requiring short amplification cycles), there is no competition/displacement between the short counter-strand of the amplicon and the detection probe, and specificity is high because the relative proportion of the internal detection region is increased with respect to the total amplicon length, allowing better differentiation between (viral) subtypes. Also, short amplicons are less likely to undergo non-specific hybridization. As a result, background is low, and short RNA sequences are more stable, with reduced tendency to form secondary structures. AAX23968-69 and AAX24035-37 are PCR primers and probes used in the method of the invention.

SQ Sequence 24 BP; 6 A; 6 C; 8 G; 4 T; 0 other;

Query Match
Best Local Similarity 100.0%; Score 24; DB 20; Length 24;
Matches 24; Conservative 0; Mismatches 0; Indels 0; *Gaps 0;

Oy 1 gcagaaggcttgcgtatggcgt 24
||| ||||| ||||| ||||| |||||
Db 1 gcagaaggcttgcgtatggcgt 24

RESULT 12

AAD19056
ID AAD19056 standard; DNA; 24 BP.

AC AAD19056;
XX
DT 18-DEC-2001 (first entry)

DE Hepatitis viral DNA amplifying forward PCR primer #30.
XX
KW Hepatitis virus; bacterial infection; fungi; protozoa; PCR primer;
KW amplification; blood-borne pathogen; sexually transmitted disease;
KW respiratory disease; ss.

OS Hepatitis virus.
XX
PN WO200168921-A2.
XX
PD 20-SEP-2001.

PP 14-MAR-2001; 2001WO-US08110.
PR 14-MAR-2000; 2000US-189344P.
PA (INVE-) INVESTIGEN.
XX
PI Koshinsky H, Zwick MS, McCue KF;
XX

DR WPI; 2001-611396/70.

XX
PT Simultaneous detection of biological entities such as bacteria, fungi and viruses by specific nucleic acid amplification -

XX
PS Disclosure; Page 31; 55pp; English.

CC The invention relates to a method and apparatus for the simultaneous detection of multiple biological entities such as bacteria, fungi and viruses by specific nucleic acid amplification. The invention also relates to a kit for simultaneous detection of biological entities. The kit is employed for detecting blood-borne pathogens, associated with a variety of infectious diseases such as respiratory and sexually transmitted diseases. The methods and apparatus are used for the simultaneous detection of biological entities present in biological and environmental samples. In particular, they are used for monitoring diseases caused by microorganisms associated with a respiratory or sexually transmitted disease such as a bacterium (*Staphylococcus*, *Pneumococcus*, *Gonococcus*, *Haemophilus*, *Bacterioides*, *Escherichia* or *Salmonella*), virus (DNA or RNA virus, such as *adenovirus*, *adeno-associated virus*, *HAV*, *HSV*, *HDV*, *HEV*, *HGV* or *TTV*), fungus (*Aspergillus fumigatus*, *Blastomycosis*, *Candida albicans*) or protozoa (*Entamoeba histolytica*). The present sequence is a PCR primer used for amplifying Hepatitis viral DNA.

XX
SQ Sequence 24 BP; 6 A; 6 C; 8 G; 4 T; 0 other;

Query Match
Best Local Similarity 100.0%; Score 24; DB 22; Length 24;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 gcagaaggcttgcgtatggcgt 24
||| ||||| ||||| |||||
Db 1 gcagaaggcttgcgtatggcgt 24

RESULT 13

AAH25403
ID AAH25403 standard; DNA; 24 BP.

AC AAH25403;
XX
DT 22-AUG-2001 (first entry)

DE PCR primer used to amplify a HCV DNA fragment.

XX
KW Magnetic glass particle; nucleic acid purification; PCR primer; ss,
XX
OS Hepatitis C virus.

XX
PN WO200137291-A1.

PD 25-MAY-2001.

PP 17-NOV-2000; 2000WO-EPI1459.

PR 17-NOV-1999; 99EP-0122833.

PR 12-MAY-2000; 2000EP-011015.

PR (HOFF) ROCHE DIAGNOSTICS GMBH.

XX
PI Weindel K, Riedling M, Geiger A;

XX
DR WPI; 2001-381247/40.

PT Novel composition of magnetic glass particles for purification of DNA or RNA in automated processes

XX
PS Example 7; Page 94; 105pp; English.

XX
CC The specification describes a composition of magnetic glass particles, which contain at least one magnetic object with a mean diameter between

RESULT 16
 ID AAT67193 standard; DNA; 26 BP.
 AC XX
 XX AAT67193;
 DT 13-FEB-1998 (first entry)
 DE Hepatitis C virus (HCV) RNA amplification primer ST280A.
 KW Hepatitis C virus; HCV; ST280A; reverse transcription PCR; RT-PCR;
 PCR primer; ss.
 OS Synthetic.
 XX
 PN EP776981-A2.
 XX
 PD 04-JUN-1997.
 XX
 PF 21-NOV-1996; 96EP-0118704.
 XX
 PR 29-NOV-1995; 95US-0007739.
 PA (HOFF) HOFFMANN LA ROCHE & CO AG F.
 XX
 PI Tsang SY;
 XX
 WPI; 1997-291296/27.
 PT Oligonucleotide primers for hepatitis C virus RNA amplification -
 by polymerase chain reaction
 PS Claim 1; Page 11; 16pp; English.
 XX
 CC This upstream primer ST280A is used in the amplification of the
 hepatitis C virus (HCV) RNA by reverse transcription PCR. This is used
 to amplify a 250 base pair product from the 5' untranslated region of
 the HCV genome. This can be used to detect HCV in a sample with increased
 sensitivity. Amplification of HCV nucleic acid using this primer is up to
 100 times more efficient than amplification with prior art primers.
 XX
 SQ Sequence 26 BP; 7 A; 6 C; 8 G; 5 T; 0 other;

Query Match Similarity 100.0%; Score 24; DB 18; Length 26;
 Best Local Similarity 100.0%; Pred. No. 7e-05; Mismatches 0; Indels 0; Gaps 0;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 gcagaaaggctgtccatggcg 24
 YY 1 ||||||| ||||| ||||| |||||
 Db 1 gcagaaggctcttagccatgcgt 24

RESULT 17
 ID AAV29058 standard; DNA; 26 BP.
 AC XX
 XX AAV29058;
 DT 07-JAN-1999 (first entry)
 DE Primer ST280A for HCV fragment.
 KW PCR primer; HCV; nucleic acid amplification; ss.
 OS Synthetic.
 OS Human cytomegalovirus.

XX
 FN modified_base 26 Location/Qualifiers
 FT /*tag= a
 FT /note= "derivatisatation with a p-(t-butyl)benzyl-residue"
 XX
 PN WO200137291-A1.
 XX
 PD 25-MAY-2001.
 XX
 PF 17-NOV-2000; 2000WO-EP11459.
 XX
 PR 17-NOV-1999; 99EP-0122853.

FT /note= "optionally benzylated, methylated, or
 nitrobenzylated"
 FT
 XX EP866071-A2.
 PN XX
 PD 23-SEP-1998.
 XX
 PF 12-MAR-1998; 98EP-0104461.
 XX
 PR 20-MAR-1997; 97US-0041127.
 XX
 PA (HOFF) HOFFMANN LA ROCHE & CO AG F.
 PI Will SG, Young KKY;
 XX
 DR WPI; 1998-482929/42.
 XX
 PT Oligo-nucleotide(s) containing N-substituted nucleotide - useful as
 primers for nucleic acid amplification
 XX
 PS Example 6; Page 16; 38pp; English.
 XX
 CC This sequence represents a primer for a fragment of HCV, and is an
 example of an oligonucleotide of the invention. The oligonucleotides of
 the invention are of the formula 5'-S1-Nu-3', or 5'-Nu-S1-3', where
 S1 is a sequence of 5-50 nucleotides; S2 is a sequence of 1-3
 nucleotides; and Nu is a nucleotide with a purine or pyrimidine base
 having an exocyclic amino group substituted by CH(R2); R1, R2 are H,
 1-10C alkyl, alkoxy, optionally substituted phenyl, phenoxy or optionally
 substituted naphthyl. The oligonucleotides are useful as primers for
 nucleic acid amplification, preferably by polymerase chain reaction. Use
 of the modified primers reduces non-specific amplification, especially
 primer dimer formation, with a concomitant increase in the yield of the
 intended target.
 XX
 SQ Sequence 26 BP; 7 A; 6 C; 8 G; 5 T; 0 other;

Query Match Similarity 100.0%; Score 24; DB 19; Length 26;
 Best Local Similarity 100.0%; Pred. No. 7e-05; Mismatches 0; Indels 0; Gaps 0;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 gcagaaaggctcttagccatgcgt 24
 YY 1 ||||||| ||||| ||||| |||||
 Db 1 gcagaaggctcttagccatgcgt 24

RESULT 18
 ID AAH25413 standard; DNA; 26 BP.
 AC XX
 AC AAH25413;
 DT 22-AUG-2001 (first entry)
 DE Forward PCR primer used to amplify a HCV DNA fragment.
 KW Magnetic glass particle; nucleic acid purification; PCR primer; ss.
 OS Hepatitis C virus.
 XX
 FN Key Location/Qualifiers
 FT modified_base 26
 FT /*tag= a
 FT /note= "derivatisatation with a p-(t-butyl)benzyl-residue"
 XX
 PN WO200137291-A1.
 XX
 PD 25-MAY-2001.
 XX
 PF 17-NOV-2000; 2000WO-EP11459.
 XX
 PR 17-NOV-1999; 99EP-0122853.

PR 12-MAY-2000; 20000P-0110165.
 XX
 PA (HOFF) ROCHE DIAGNOSTICS GMBH.
 XX
 PI Weindel K, Riedling M, Geiger A;
 XX
 DR WPI; 2001-381247/40.
 XX
 PT Novel composition of magnetic glass particles for purification of DNA or RNA in automated processes
 XX
 PS Example 7; Page 98; 10-pp; English.
 SQ
 CC The specification describes a composition of magnetic glass particles, which contain at least one magnetic object with a mean diameter between 5-500 nm. The composition is useful for the purification of nucleic acids. The composition can be used to process large quantities of nucleic acid samples, because it does not involve the particles being centrifuged or the fluids being drawn through glass fiber filters.
 CC PCR primers AAH2413-14 were used to amplify HCV DNA fragments. The amplified fragment can be purified using the method of the invention.
 CC Sequence 26 BP; 7 A; 6 C; 8 G; 5 T; 0 other;
 XX
 CC Query Match 100.0%; Score 24; DB 22; Length 26;
 CC Best Local Similarity 100.0%; Pred. No. 7e-05; 0; Mismatches 0;
 CC Matches 24; Conservative 0; Indels 0; Gaps 0;
 CC Oy 1 gcagaaagcgctggcattgggt 24
 CC Db 1 gcagaaagcgctggcattgggt 24
 RESULT 19
 ID AAS10490
 ID AAS10490 standard; RNA; 77 BP.
 AC AAS10490;
 DT 24-OCT-2001 (first entry)
 XX
 DE HCV 5'-UTR domain II EMSA RNA probe.
 XX
 DE HCV 5' UTR; minimal IRES; internal ribosome entry site; eIF3;
 KW eukaryotic initiation factor 3; HCV translation initiation; antiviral;
 KW RNA electrophoretic gel mobility shift assay; EMSA; ss.
 XX
 OS Hepatitis C virus strain 1a M67463.
 XX
 Key Location/Qualifiers
 FT misc_binding 1..5
 FT /*tag= a
 FT /bound_moiety= "Forms double stranded region with
 FT bases 73-77"
 FT stem_loop 8..22
 FT /*tag= C Designated as 11a"
 FT /note= 23..28
 FT misc_binding /*tag= b
 FT /bound_moiety= "Forms double stranded region with
 FT bases 60-55"
 FT stem_loop 32..50
 FT /*tag= C /note= "Designated as 11b"
 FT misc_binding 55..60
 FT /*tag= d /bound_moiety= "Forms double stranded region with
 FT bases 28-23"
 FT misc_binding 73..77
 FT /*tag= e /bound_moiety= "Forms double stranded region with
 FT bases 51"
 XX
 PN WO200144266-A2.
 XX
 PR 21-JUN-2001.
 PD 22-DEC-1999; 99US-0171804.
 XX
 PR 18-DEC-2000; 2000WO-GB04862.
 XX
 PR 16-DEC-1999; 99GB-0029820.
 XX
 PR 16-DEC-1999; 99US-0171804.
 XX
 PA (RIBO-) RIBOTARGETS LTD.
 XX
 PI Karn J, Walker S;
 XX
 DR WPI; 2001-465050/50.
 XX
 PT Nucleotide sequences derived from Hepatitis C virus, useful for identifying candidate antiviral compounds -
 XX
 PS Disclosure; Fig 5E; 48pp; English.
 CC The present sequence represents Hepatitis C virus (HCV) 5'-UTR domain II RNA probe used in a RNA electrophoretic gel mobility shift assay (EMSA). The present sequence is described in an invention relating to a novel compound comprising nucleotide sequences capable of annealing and which is derived from a 5'-untranslated region (UTR) of HCV which is essential for binding of eif3 (eukaryotic initiation factor 3). The invention particularly relates to a sub-region of the HCV 5'-UTR referred to as the minimal internal ribosome entry site (MRES) which can be used to identify drugs which inhibit HCV translation initiation. The compounds of the invention may be used to screen for potential HCV antiviral compounds. Assays based on the MRES enable potential antivirals to be screened in a cheaper and easier way. It allows rapid assaying with a small volume of material and are suitable to parallel processing.
 CC Sequence 77 BP; 16 A; 20 C; 23 G; 18 U; 0 other;
 XX
 CC Query Match 100.0%; Score 24; DB 22; Length 77;
 CC Best Local Similarity 83.3%; Pred. No. 6.9e-05; 0; Mismatches 0;
 CC Matches 20; Conservative 4; Indels 0; Gaps 0;
 CC Oy 1 gcagaaagcgctggcattgggt 24
 CC Db 26 gcagaaagcgcuauccauuggcu 49
 RESULT 20
 ID AAQ85920
 ID AAQ85920 standard; DNA; 37 BP.
 XX
 AC AAQ85920;
 DT 02-NOV-1995 (first entry)
 XX
 DE Hepatitis C virus genome internal PCR primer YK-103U.
 KW Hepatitis C virus; HCV; non-A non-B; external PCR primer; YK-103U; primer specific detection; ss.
 XX
 OS Synthetic.
 XX
 Key Location/Qualifiers
 FT misc_feature 1..13
 FT /*tag= a /note= "Oligo (dU) sequence"
 FT /note= "Oligo (dU) sequence"
 XX
 PN WO9506753-A.
 XX
 PD 09-MAR-1995.
 XX
 PR 02-SER-1994; 94WO-US09869.
 PF

XX
 PR 03-SEP-1993; 93US-0116344.
 XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX
 PI Fields HA, Khudyakov YE;
 XX
 DR WPI; 1995-115465/15.
 XX
 PT New method and kit for primer-specific detection of nucleic acids
 PT - using two primers having a known sequence and a marker, resp
 PT for solid phase detection of amplification prods.
 XX
 PS Example 1; Page 12; 20pp; English.
 XX
 AAQ85918/19 are external, and AAQ85820/21 are internal PCR primers for
 CC the Hepatitis C virus (HCV) genome. They were used to demonstrate
 CC a new method for the primer specific detection of nucleic acids.
 XX
 Sequence 37 BP; 6 A; 6 C; 7 G; 5 T; 0 other;
 Query Match 95.8%; Score 23; DB 16; Length 37;
 Best Local Similarity 100.0%; Pred. No. 0.00027;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 cagaaaagcgcttagccatggcgt 24
 Db 14 cagaaaagcgcttagccatggcgt 36

RESULT 21
 AAQ75035 standard; DNA; 37 BP.
 XX
 AC AAQ75035;
 XX
 DT 04-AUG-1995 (first entry)
 XX
 DE PCR primer for the amplification of a peptide-streptavidin-oligo.
 XX
 KW Synthetic peptide; solid phase immunoassay; ss.
 OS Synthetic.
 XX
 OS Synthetic.
 XX
 FT misc_difference 1
 FT /*tag= a
 FT /note= "linked to biotin"
 XX
 PN WO9426932-A.
 XX
 PD 24 -NOV-1994.
 XX
 PF 13-MAY-1994; 94WO-US05407.
 XX
 PR 13-MAY-1993; 93US-0061694.
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX
 PI Fields HA, Khudyakov YE;
 XX
 DR WPI; 1995-006819/01.
 XX
 PT Solid phase immunoassay using oligo:nucleotide as label - also
 PT new conjugates of oligo:nucleotide coupled to antigenic peptide,
 PT partic. for diagnosing hepatitis C or E virus infection
 XX
 PS Example; Page 18; 34pp; English.
 XX
 CC AAR62941 and AAR62942 are examples of synthetic immunoreactive peptides.
 CC They are used in a method for detecting an antigen in a subject. The
 CC method involves binding the antigen to a solid support and then
 CC reacting it with an immunoreactive ligand (L) bound to an oligo;
 CC removing any unreacted L, and then detecting the presence of the
 CC oligo. A similar method can be used to detect Abs, in which case the
 CC ligand is an oligo-labelled Ag. The use of an amplifiable oligo as
 CC the label allows Ag or Ab to be detected at very low levels. In the
 CC example, a synthetic peptide from the NS4 protein of the hepatitis
 CC virus with structure (AAR6243) is biotinyled using a
 CC commercially available kit. A biotinylated oligo with the structure
 CC 5'-biotinylated AAQ75035-3 was prep'd. This oligo is composed
 CC of sequences of two PCR primers seed. by a short additional
 CC sequence. The shorter the region to be amplified the better the
 CC efficiency of amplification obta. The biotinylated oligo is pre-

CC	incubated with streptavidin. Then this complex linked by biotin-streptavidin binding. This RNA complex is then used in place of chemically prep'd. oligo-peptide conjugates mentioned above.	DR	WPI; 1993-386599/48.
CC		XX	
CC		PT	Enzymatic RNA molecules - used to inhibit viral replication.
CC		PT	infection and gene expression
XX	Sequence 58 BP; 10 A; 11 C; 15 G; 22 T; 0 other;	XX	Claim 5; Fig 12; 287pp; English.
QY	2 cagaaggcgcttagccatggcgt 24	XX	The sequences (AAQ52816-052823) are pref. hepatitis C virus target sequences for enzymatic RNA molecules. The RNA molecules are complementary to a substrate binding region in the specified gene target. They also have enzymatic activity, in that they specifically cleave RNA in the target. The ERMs interfere with viral replication and therefore have anti-viral properties. They can be used to attenuate viruses to be used in vaccines.
Db	11 cagaaggcgcttagccatggcgt 33	XX	Sequence 21 BP; 6 A; 5 C; 7 G; 3 U; 0 other;
RESULT	23	XX	Query Match 95.8%; Score 23; DB 16; Length 58; Best Local Similarity 100.0%; Pred. No. 0.00027; Mismatches 23; Conservative 0; Indels 0; Gaps 0;
AAQ52817		XX	AC
AAQ52817	standard; RNA; 21 BP.	AC	
XX		AC	
AC		AC	
XX		AC	
DT	26-MAY-1994 (first entry)	XX	QY
DE	HCV target sequence 2.	XX	1 gcagaaaggcgcttagccatgg 21
XX		XX	Db
KW	RNA; enzyme; enzymatic RNA molecule; ERM; cleave; RNA; mRNA; hnRNA; picornavirus; HIV; immunodeficiency virus; hepatitis B virus; HBV; papilloma virus; HPV; Epstein-Barr virus; EBV; TCV; T-cell leukaemia virus; hepatitis C virus; HCV; cytomegalovirus; influenza virus; HSV; herpes simplex virus; vector; immune response; antibody; ribozyme; viral RNA; treatment; ss.	XX	1 gcagaaggcgccuacgcauagg 21
KW		XX	
OS	Synthetic.	XX	
XX		XX	
PN	W09323569-A.	XX	
XX		XX	
PD	25-NOV-1993.	XX	
XX		XX	
PF	29-APR-1993; 93WO-US04020.	XX	
XX		XX	
PR	11-MAY-1992; 92US-0882689.	XX	
PR	14-MAY-1992; 92US-0882712.	XX	
PR	14-MAY-1992; 92US-0882713.	XX	
PR	14-MAY-1992; 92US-0882714.	XX	
PR	14-MAY-1992; 92US-0882823.	XX	
PR	14-MAY-1992; 92US-0882824.	XX	
PR	14-MAY-1992; 92US-0882886.	XX	
PR	14-MAY-1992; 92US-0882888.	XX	
PR	14-MAY-1992; 92US-0882889.	XX	
PR	14-MAY-1992; 92US-0882890.	XX	
PR	14-MAY-1992; 92US-0882891.	XX	
PR	14-MAY-1992; 92US-0883023.	XX	
PR	14-MAY-1992; 92US-0883849.	XX	
PR	14-MAY-1992; 92US-0884073.	XX	
PR	14-MAY-1992; 92US-0884333.	XX	
PR	14-MAY-1992; 92US-0884422.	XX	
PR	14-MAY-1992; 92US-0884431.	XX	
PR	14-MAY-1992; 92US-0884436.	XX	
PR	14-MAY-1992; 92US-0884521.	XX	
PR	31-JUL-1992; 92US-0923138.	XX	
PR	26-AUG-1992; 92US-0936086.	XX	
PR	18-SEP-1992; 92US-094359.	XX	
PR	15-OCT-1992; 92US-0963322.	XX	
PR	07-DEC-1992; 92US-0987129.	XX	
PR	07-DEC-1992; 92US-0987130.	XX	
PR	07-DEC-1992; 92US-0987133.	XX	
PA	(RIBO-) RIBOZYME PHARM INC.	XX	
XX		XX	
PI	Draper KG, Dudyce LW, Holecek JJ, Macejak DG, Mamine JA;	XX	
PI	McSwiggen JA;	XX	
CC	The invention relates to methods and compositions of detection and characterisation of nucleic acid sequences and sequence changes. One method of detection and characterisation comprises: (i) providing: (1) a folded target having a DNA sequence comprising at least 1 double stranded region and at least 1 single stranded region; and (ii) at least 1 probe complementary to at least a portion of the folded target; and	XX	

(b) mixing the target and probes so that the probe hybridises to form a probe / folded target complex. Also provided are methods for determination of structure formation in nucleic acid targets; for analysing folded nucleic acids targets; and for analysis of nucleic acid structures. The methods can be used for the detection and characterisation of nucleic acid sequences to detect the presence of pathogenic nucleic acid sequences indicative of an infection, the presence of variants or alleles of mammalian genes associated with disease and cancers, and the identification of the source of nucleic acids found in forensic samples, as well as in paternity determinations. The methods allow simultaneous qualitative, quantitative and positional analysis. The methods may be performed in solution or in the solid phase (e.g. on a solid support). The methods are powerful in that they allow for analysis of longer fragments of nucleic acid than current methodologies. Sequences AAV0447-48 represent primers used for the PCR amplification of hepatitis C virus (HCV) target DNA used in the hybridisation analysis using multiple capture probes for HCV genotyping.

XX Sequence 21 BP; 6 A; 5 C; 7 G; 3 T; 0 other;

Query Match Best Local Similarity 87.5%; Score 21; Length 21;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 gcagaaagcgctcattccatgg 21

Db 1 gcaaaaaggcgcttacccatgg 21

RESULT 25

AAA72990/C ID AAA72990 standard; DNA; 21 BP.

XX AC AAA72990;

XX DT 24-NOV-2000 (first entry)

DE Hepatitis C virus antisense oligonucleotide HCV8B.

XX Hepatitis C virus; HCV; antisense oligonucleotide; leuciferinase;

KW luciferase; HepG2; medicine; ss.

OS Hepatitis C virus.

XX PN CN153138-A.

PD 17-MAY-2000.

XX PF 09-NOV-1998; 98CN-0124388.

XX PR 09-NOV-1998; 98CN-0124388.

XX (RADI-) RADIOMEDICINE ACAD MILITARY MEDICAL SCI.

XX PI Wang S, Wang X, Zhu B;

XX DR WPI; 2000-466526/41.

PT Structure and usage of antisense oligonucleotide for treating diseases correlative to hepatitis C virus

XX PS Claim 1; Page 1; 20pp; Chinese.

The present invention describes antisense oligonucleotides which are designed and synthesised on the basis of the gene structure of hepatitis C virus (HCV) and can be used to suppress the expression of HCV gene. The non-coding region 5' of HCV gene is used to regulate the instantaneous expression system of leuciferinase gene in HepG2 cells and the transgenic cell model HepG2.9706 of luciferase gene. The 15 antisense oligonucleotides (AAA72988 to AAA73002) which are complementary

CC to the non-coding region 5' and translational initiation region of HCV CC are actively screened and evaluated to discover for the first time the CC oligonucleotides HCV279, HCV49, HCV363, HCV313 and their CC chemical modified objects for suppressing the expression of HCV gene. CC Thus, the present invention relates to the new medicine for treating the CC diseases associated with HCV.

XX Sequence 21 BP; 3 A; 7 C; 5 G; 6 T; 0 other;

Query Match Best Local Similarity 87.5%; Score 21; DB 21; Length 21;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 gcagaaagcgctcattccatgg 21

Db 21 GCAGAAAGCCTAGCCATCG 1

RESULT 26

AAH79078 ID AAH79078 standard; DNA; 21 BP.

XX AC AAH79078;

XX DT 20-NOV-2001 (first entry)

DE HCV negative strand RNA sense PCR primer.

XX KW Transgenic animal model; human hepatotrophic pathogen; immunotherapy; human hepatitis C virus; HCV; vaccine; antiviral; hyperlipidaemia; atherosclerosis; PCR primer; ss.

XX OS Hepatitis C virus.

XX OS Syntactic.

XX PN WO200167854-A1.

XX PD 20-SEP-2001.

XX PP 16-MAR-2001; 2001WO-CA00350.

XX PR 17-MAR-2000; 2000US-0528120.

XX PA (KNET /) KNETEMAN N M.

PA (TYR /) TYRELL D L.

PA (MERC /) MERCER D F.

XX PT Kneteman NM, Tyrrell DL, Mercer DF;

XX DR WPI; 2001-582308/65.

XX PT New chimeric immunodeficient transgenic murine host susceptible to hepatitis C virus infection, useful as model for screening compounds, comprises chimeric liver, where transgene encodes urokinase-type plasminogen activator

XX PS Example 4; Page 38; 78pp; English.

CC The invention relates to a non-human animal model that is susceptible to CC infection by human hepatotropic pathogens, especially human hepatitis C CC virus (HCV). The model is based on a non-human, immunocompromised CC xenogeneic transgenic animal having a human-mouse chimeric liver. The CC invention outlines the creation of a chimeric immunodeficient murine host CC infected with human HCV and deficient in functional syngeneic B and T CC lymphocytes, comprising a genetically integrated transgene encoding a CC urokinase-type plasminogen activator in liver cells and a chimeric liver CC comprising human hepatocytes engrafted into liver of the murine host, CC where inoculation of chimeric host with HCV results in HCV infection. The CC chimeric mouse model is useful for culturing human HCV, for screening CC candidate agents for activity against a hepatotropic pathogen, especially a vaccine for active immunotherapy or for therapeutic vaccination or an immunotherapeutic agent e.g. anti-HCV body or

Query Match 87.5%; Score 21; DB 22; Length 24;
 Best Local Similarity 100.0%; Pred. No. 0.004; Mismatches 0;
 Matches 21; Conservative 0; Indels 0; Gaps 0;

Qy 4 gaatggcttagccatgggt 24
 |||||||
 Db 1 gaatggcttagccatgggt 21

RESULT 29
 AAQ98291

ID AAQ98291 standard; DNA; 25 BP.

XX
 AC AAQ98291;

XX
 DT 19-MAR-1996 (first entry)

XX
 DE Hepatitis C virus sense PCR detection primer P21.

XX
 KW Primer; hepatitis C virus; PCR; amplification; reverse transcription;

KW detection; non-translated region; ss.

XX
 OS Synthetic.

XX
 PN JP07184695-A.

XX
 PD 25-JUL-1995.

XX
 PP 27-DEC-1993; 93JP-0332682.

XX
 PR 27-DEC-1993; 93JP-0332682.

XX
 PA (SANNWA KAGAKU KENKYUSHO CO LTD.

DR XX
 WPI: 1995-287992/38.

XX
 PT Simple detection of Hepatitis C virus in a single reaction tube - useful for high sensitivity and ease of reproduction.

XX
 PS Example 3; Page 7; 14pp; Japanese.

CC The primers AAQ98270-94 are used in a novel simple method for the detection of hepatitis C virus. The novel method involves the steps of extracting the virus from a sample, synthesising cDNA from the viral RNA by reverse transcription, amplifying the cDNA by a first PCR and reamplifying the amplified product in a second PCR, all of which occur in a single reaction tube. The primers are designed based on a 334 bp sequence (AAQ98272) derived from a 5' non-translated region of the viral genome. This primer corresponds to bases 54-78 of AAQ98272.

XX Sequence 25 BP; 6 A; 5 C; 8 G; 6 T; 0 other;

SQ Query Match 87.5%; Score 21; DB 16; Length 25;
 Best Local Similarity 100.0%; Pred. No. 0.004; Mismatches 0;
 Matches 21; Conservative 0; Indels 0; Gaps 0;

Qy 4 gaatggcttagccatgggt 24
 |||||||
 Db 1 gaatggcttagccatgggt 21

search completed: August 26, 2002, 22:24:55
 Job time: 6234 sec

GenCore version 4.5
 Copyright (c) 1993 - 2000 Compugen Ltd.
 OM nucleic - nucleic search, using sw model
 Run on : August 26, 2002, 19:12:26 ; Search time 1915.63 Seconds
 (without alignments)
 (262 178 million cell matches/sec)

Title: US-10-037-990A-1
 Perfect score: 24
 Sequence: 1 gagaagaaggctttagccatggcgt 24
 Scoring table: <Oligo_NUC
 Gapop 60.0 , Gapext 60.0
 Searched: 1797556 seqs, 10463268293 residues
 Word size : 21
 Total number of hits satisfying chosen parameters: 25
 Minimum DB seq length: 0
 Maximum DB seq length: 100
 L399768 Sequence 7
 AR8054575 Sequence 7
 AR094137 Sequence
 AX147021 Sequence
 AX12147 Sequence 6
 AX021612 Sequence
 AX0172761 Sequence
 BD000263 Oligonucleic
 AR131532 Sequence
 AR144109 Sequence
 AX250669 Sequence
 BD001049 Method an
 BD001478 Method an
 AX250672 Sequence

Post-processing: Listing first 65 summaries

ALIGNMENT

RESULT	1	gb_ba:*						
LOCUS	A68287	gb_htg:*						
DEFINITION	A68287	Sequence 8 from Patent WO9746716.	24 bp	DNA	Linear	PAT	06-MAY-1999	
ACCESSION	A68287							
VERSION	A68287.1							
KEYWORDS								
SOURCE								
ORGANISM		unidentified						
REFERENCE		unclassified.						
1.	(bases 1 to 24)							
AUTHORS	Bosio,P., Strumia,C. and Clemenza,F.							
TITLE	METHOD TO DETECT HCV SPECIFIC NUCLEIC ACIDS							
JOURNAL	Patent: WO 9746716-A 8 NOV-1997;							
COMMENT	WABCO B V (NL)							
FEATURES	Other publication IT RM560404 19971209.							
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ORIGIN		/ab_xref="taxon:32644"						
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24	24	ggagaaggcgctatgcattgggt	Similarity	0;	Mismatches 0;			
28:	em_sts:*	ggagaaggcgctatgcattgggt	Conservative	0;	Indels 0;			
29:	em_un:*	ggagaaggcgctatgcattgggt	Matches	0;	Gaps 0;			
30:	em_vl:*	ggagaaggcgctatgcattgggt	24					
31:	em_htg_hum:*	ggagaaggcgctatgcattgggt						
32:	em_htg_inv:*	ggagaaggcgctatgcattgggt						
33:	em_htg_other:*	ggagaaggcgctatgcattgggt						
em_htg_inv:*								
RESULT	2							
AR054578	AR054578							
LOCUS	AR054578							
DEFINITION	Sequence 4 from patent US 5837442.	24 bp	DNA	Linear	PAT	29-SEP-1999		
ACCESSION	AR054578							
VERSION	AR054578.1							
KEYWORDS								
SOURCE	Unknown.							
ORGANISM	Unclassified.							
SUMMARIES								
Result No.	Score	Query Match Length DB ID	description					

REFERENCE 1 (bases 1 to 24)
 AUTHORS Tsang,S.Yen.
 TITLE Oligonucleotide primers for amplifying HCV nucleic acid
 JOURNAL Patent: US 583742-A 4 17-NOV-1998;
 FEATURES /organism="unknown"
 SOURCE 1..24
 BASE COUNT 6 a 6 c 8 g 4 t
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Query Match 100.0%; Score 24; DB 6; Length 24;
 Best Local Similarity 100.0%; Pred. No. 0.0018; Mismatches 0; Indels 0; Gaps 0;
 Matches 24; Conservative 0; MisMatches 0;

QY 1 gcagaagcgtctggccatgggt 24
 LOCUS AX003941 Sequence 1 from Patent WO92323249.
 DEFINITION 24 bp DNA linear PAT 07-SEP-2000
 ACCESSION AX003941
 VERSION AX003941.1 GI:9927601
 KEYWORDS synthetic construct.
 SOURCE
 ORGANISM artificial sequence.

REFERENCE 1 (bases 1 to 24)
 AUTHORS Kessler,C., Bartl,K., Haberhausen,G. and Orum,H.
 TITLE Specific and sensitive method for detecting nucleic acids
 JOURNAL Patent: WO 9923249-A 1 14-MAY-1999;
 KESSLER CHRISTOPH (DE); BARTL KNUST (DE); HABERHAUSEN GERD (DE);
 ROCHE DIAGNOSTICS GMBH (DE); ORUM HENRIK (DK)
 FEATURES Location/Qualifiers
 SOURCE 1..24
 /organism="synthetic construct"
 /note="taxon:32630"
 /db_xref="taxon:32630"

FEATURES source

BASE COUNT 6 a 6 c 8 g 4 t
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 Best Local Similarity 100.0%; Pred. No. 0.0018; Mismatches 0; Indels 0; Gaps 0;
 Matches 24; Conservative 0; MisMatches 0; Indels 0; Gaps 0;

QY 1 gcagaagcgtctggccatgggt 24
 LOCUS AX003941 Sequence 1 from Patent WO92323249.
 DEFINITION 24 bp DNA linear PAT 07-SEP-2000
 ACCESSION AX003941
 VERSION AX003941.1 GI:9927601
 KEYWORDS synthetic construct.
 SOURCE
 ORGANISM Hepatitis C virus.

REFERENCE 1 (bases 1 to 24)
 AUTHORS Kessler,C., Bartl,K., Haberhausen,G. and Orum,H.
 TITLE Specific and sensitive method for detecting nucleic acids
 JOURNAL Patent: WO 9923250-A 1 14-MAY-1999;
 KESSLER CHRISTOPH (DE); BARTL KNUST (DE); HABERHAUSEN GERD (DE);
 ROCHE DIAGNOSTICS GMBH (DE); ORUM HENRIK (DK)
 FEATURES Location/Qualifiers
 SOURCE 1..24
 /organism="Hepatitis C virus"
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 /note="taxon:11103"
 /db_xref="taxon:32630"

FEATURES source

BASE COUNT 6 a 6 c 8 g 4 t
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Query Match 100.0%; Score 24; DB 6; Length 24;
 Best Local Similarity 100.0%; Pred. No. 0.0018; Mismatches 0; Indels 0; Gaps 0;
 Matches 24; Conservative 0; MisMatches 0;

QY 1 gcagaagcgtctggccatgggt 24
 LOCUS AX021563 Sequence 1 from Patent WO924606.
 DEFINITION 24 bp DNA linear PAT 07-SEP-2000
 ACCESSION AX021563
 VERSION AX021563.1 GI:10044847
 KEYWORDS Hepatitis C virus.
 SOURCE Hepatitis C virus.
 ORGANISM Hepatitis C virus.

REFERENCE 1 (bases 1 to 24)
 AUTHORS Kessler,C., Bartl,K., Haberhausen,G. and Orum,H.
 TITLE Specific and sensitive nucleic acid detection method
 JOURNAL Patent: WO 9924606-A 1 20-MAY-1999;
 KESSLER CHRISTOPH (DE); BARTL KNUST (DE); HABERHAUSEN GERD (DE);
 ROCHE DIAGNOSTICS GMBH (DE); ORUM HENRIK (DK)

FEATURES Location/Qualifiers
 SOURCE 1..24
 /organism="synthetic construct"
 /db_xref="taxon:32630"
 /note="Synthetic oligonucleotide primer (HCV forward)"

FEATURES source

BASE COUNT 6 a 6 c 8 g 4 t
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		DEFINITION	Sequence 17 from patent US 5561058.					
		ACCESSION	I26949					
		VERSION	I26949.1					
		KEYWORDS						
		SOURCE	Unknown.					
		ORGANISM	Unknown.					
		REFERENCE	Unclassified.					
		AUTHORS	1 (bases 1 to 24)					
		TITLE	Gelfand,D.H., Myers,T.W. and Sigtuna,C.L.					
		JOURNAL	Methods for coupled high temperatures reverse transcription and polymerase chain reactions					
		FEATURES	patent: US 5561058-A 17 OCT-1996; Location/Qualifiers					
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		BASE COUNT	6 a 6 c 8 g 4 t					
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		LOCUS	140301					
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		ACCESSION	I40301					
		VERSION	I40301.1					
		KEYWORDS						
		SOURCE	Unknown.					
		ORGANISM	Unknown.					
		REFERENCE	Unclassified					
		AUTHORS	1 (bases 1 to 24)					
		TITLE	Lin,L., Cimino,G. and Zhu,Y.S.					
		JOURNAL	Nucleic acid preparation methods					
		FEATURES	patent: US 5620852-A 9 APR-1997; Location/Qualifiers					
		SOURCE	1. .24					
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		SOURCE	Unknown.					
		ORGANISM	Unknown.					
		REFERENCE	Unclassified.					
		AUTHORS	1 (bases 1 to 24)					
		TITLE	Resnick,R.M. and Young,K.K.Y.					
		JOURNAL	Methods, primers and probes for detection of hepatitis C and novel variants					
		FEATURES	Patent: US 5527669-A 18 JUN-1996; Location/Qualifiers					
		SOURCE	1. .24					
		BASE COUNT	6 a 6 c 8 g 4 t					
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		AUTHORS	1 (bases 1 to 24)					
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AUTHORS	Lin,L.	Qy	1	gcagaaggcttagccatggcg	24					
TITLE	Nucleic acid preparation methods									
JOURNAL	US 5564179 A 9 Aug-1997;	Db	1	GCAGAAAGCGCTAGCCATGGCGT	24					
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LOCUS	168634		24 bp	DNA	linear	PAT 04-FEB-1998				
DEFINITION	Sequence 7 from patent US 5677124.									
ACCESSION	168634									
VERSION	168634.1									
KEYWORDS										
SOURCE	Unknown.									
ORGANISM	Unclassified.									
REFERENCE	1 (bases 1 to 24)									
AUTHORS	Dubois,D.B., Winkler,M.M. and Pasloske,B.L.									
TITLE	Ribonuclease resistant viral RNA standards									
JOURNAL	Patent: US 5677124 A 7 14-Oct-1997;									
FEATURES	Location/Qualifiers									
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BASE COUNT	6 a	6 c	8 g	4 t						
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DEFINITION	Sequence 3 from patent US 6001611.									
ACCESSION	AR094137									
VERSION	AR094137.1									
KEYWORDS	Unknown.									
SOURCE	Unclassified.									
REFERENCE	1 (bases 1 to 26)									
AUTHORS	Will,S.Gordon.									
TITLE	Modified nucleic acid amplification primers									
JOURNAL	Patent: US 6001611-A 3 14-DEC-1999;									
FEATURES	Location/Qualifiers									
source	1..26									
BASE COUNT	7 a	6 c	8 g	5 t						
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ACCESSION	AX147021									
VERSION	AX147021.1									
KEYWORDS										
SOURCE	synthetic construct.									
ORGANISM	artificial sequence.									
REFERENCE	1 (bases 1 to 26)									
AUTHORS	Weindel,K., Riedling,M. and Geiger,A.									
TITLE	Magnetic glass particles, method for their preparation and uses thereof									
JOURNAL	Patent: WO 0137291-A 15 25-MAY-2001;									
FEATURES	Roche Diagnostics GmbH (DE)									
source	Location/Qualifiers									
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VERSION	AX147021.1									
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SOURCE	synthetic construct.									
ORGANISM	artificial sequence.									
REFERENCE	1 (bases 1 to 26)									
AUTHORS	Tsang,S.Yen.									
TITLE	Oligonucleotide primers for amplifying HCV nucleic acid									
JOURNAL	Patent: US 5837442-A 17-NOV-1998;									
FEATURES	Location/Qualifiers									
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BASE COUNT	7 a	6 c	8 g	5 t						
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ACCESSION	AR094137									
VERSION	AR094137.1									
KEYWORDS	Unknown.									
SOURCE	Unclassified.									
REFERENCE	1 (bases 1 to 26)									
AUTHORS	Will,S.Gordon.									
TITLE	Modified nucleic acid amplification primers									
JOURNAL	Patent: US 6001611-A 3 14-DEC-1999;									
FEATURES	Location/Qualifiers									
source	1..26									
BASE COUNT	7 a	6 c	8 g	5 t						
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DEFINITION	Sequence 3 from patent US 6001611.									
ACCESSION	AR094137									
VERSION	AR094137.1									
KEYWORDS	Unknown.									
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AUTHORS	Will,S.Gordon.									
TITLE	Modified nucleic acid amplification primers									
JOURNAL	Patent: US 6001611-A 3 14-DEC-1999;									
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AUTHORS	Will,S.Gordon.									
TITLE	Modified nucleic acid amplification primers									
JOURNAL	Patent: US 6001611-A 3 14-DEC-1999;									
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VERSION	AR094137.1									
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SOURCE	Unclassified.									
REFERENCE	1 (bases 1 to 26)									
AUTHORS	Will,S.Gordon.									
TITLE	Modified nucleic acid amplification primers									
JOURNAL	Patent: US 6001611-A 3 14-DEC-1999;									
FEATURES	Location/Qualifiers									
source	1..26									
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VERSION	AR094137.1									
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AUTHORS	Will,S.Gordon.									
TITLE	Modified nucleic acid amplification primers									
JOURNAL	Patent: US 6001611-A 3 14-DEC-1999;									
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ACCESSION	AR094137									
VERSION	AR094137.1									
KEYWORDS	Unknown.									
SOURCE	Unclassified.									
REFERENCE	1 (bases 1 to 26)									
AUTHORS	Will,S.Gordon.									
TITLE	Modified nucleic acid amplification primers									
JOURNAL	Patent: US 6001611-A 3 14-DEC-1999;									
FEATURES	Location/Qualifiers									
source	1..26									
BASE COUNT	7 a	6 c	8 g	5 t						
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ACCESSION	AR094137									
VERSION	AR094137.1									
KEYWORDS	Unknown.									
SOURCE	Unclassified.									
REFERENCE	1 (bases 1 to 26)									
AUTHORS	Will,S.Gordon.									
TITLE	Modified nucleic acid amplification primers									
JOURNAL	Patent: US 6001611-A 3 14-DEC-1999;									
FEATURES	Location/Qualifiers									
source	1..26									
BASE COUNT	7 a	6 c	8 g	5 t						
ORIGIN										
RESULT	15									
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ACCESSION	AR094137									
VERSION	AR094137.1									
KEYWORDS	Unknown.									
SOURCE	Unclassified.									
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AUTHORS	Will,S.Gordon.									
TITLE	Modified nucleic acid amplification primers									
JOURNAL	Patent: US 6001611-A 3 14-DEC-1999;									
FEATURES	Location/Qualifiers									
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RESULT	15									
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ACCESSION	AR094137									
VERSION	AR094137.1									
KEYWORDS	Unknown.									
SOURCE	Unclassified.									
REFERENCE	1 (bases 1 to 26)									
AUTHORS	Will,S.Gordon.									
TITLE	Modified nucleic acid amplification primers									
JOURNAL	Patent: US 6001611-A 3 14-DEC-1999;		</td							

RESULT	16
LOCUS	I22147
DEFINITION	Sequence 6 from Patent US 5527669.
ACCESSION	I22147
VERSION	I22147..1 GI:1602501
KWWORDS	ORGANISM Unknown.
SOURCE	Unclassified.
REFERENCE	1 (bases 1 to 26)
AUTHORS	Resnick,R.M and Young,K.K.Y.
TITLE	Methods, primers and probes for detection of hepatitis C and novel variants
JOURNAL	Patent: US 5527669-A 6 JUN-1996;
FEATURES	Location/Qualifiers 1..26 /organism="unknown"
BASE COUNT	7 a 7 c 8 g 4 t
ORIGIN	
RESULT	17
LOCUS	AX021612
DEFINITION	Sequence 50 from Patent WO9924606.
ACCESSION	AX021612
VERSION	AX021612..1 GI:1004896
KEYWORDS	
SOURCE	Hepatitis C virus.
ORGANISM	Hepatitis C viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae; Hepacivirus.
REFERENCE	1 (bases 1 to 51)
AUTHORS	Kessler,C., Bartl,K., Haberhausen,G. and Orum,H.
TITLE	Specific and sensitive nucleic acid detection method
JOURNAL	Patent: WO 9924606-A 50 20-MAY-1999;
KESSLER CHRISTOPH (DE); BARTL KNUT (DE); HABERHAUSEN GERD (DE); ROCHE DIAGNOSTICS GMBH (DE); ORUM HENRIK (DK)	
FEATURES	Location/Qualifiers 1..51 /organism="Hepatitis C virus"
BASE COUNT	11 a 12 c 15 g 13 t
ORIGIN	
RESULT	18
LOCUS	AX127261
DEFINITION	Sequence 9 from Patent WO0144266.
ACCESSION	AX127261
VERSION	AX127261..1 GI:14597857
KWWORDS	ORGANISM Synthetic construct.
SOURCE	Artificial sequence.
REFERENCE	1 (bases 1 to 77)
AUTHORS	Karn,J.C. and Walker,S.C.
TITLE	Nucleic acid compounds and screening assays using the same
JOURNAL	Patent: WO 014266-A 9 21-JUN-2001;
KWWORDS	Ribotargets Limited (GB)
SOURCE	Location/Qualifiers 1..77 /organism="synthetic construct" /db_xref="taxon:32630" /note="Probe"
FEATURES	/db_xref="taxon:32630" /note="Probe"
BASE COUNT	16 a 20 c 23 g 18 t
ORIGIN	
RESULT	19
LOCUS	BD000263
DEFINITION	Oligonucleotide primers for efficient detection of hepatitis C virus (HCV) and methods of use thereof.
ACCESSION	BD000263
VERSION	BD000263..1 GI:18623342
KEYWORDS	JP 200279200-A/1.
SOURCE	Synthetic construct.
ORGANISM	Artificial sequence.
REFERENCE	1 (bases 1 to 28)
AUTHORS	Lynen,J.M. and Gorman,K.M.
TITLE	Oligonucleotide primers for efficient detection of hepatitis C virus (HCV) and methods of use thereof
JOURNAL	Patent: JP 200279200-A 1 10-OCT-2000;
COMMENT	ORTHO CLINICAL DIAGNOSTICS INC
OS	Artificial Sequence
PN	JP 200279200-A/1
PD	10-OCT-2000
PF	03-FEB-2000
PR	03-FEB-1999 US 60/118497
PI	JEFFREY M LYNN,KEVIN M GORMAN
PC	C12Q1/68,C12N15/09//C12N15/09,C12R1..92),C12N15/00,(C12N15/00, C12R1..92)
CC	
FR	Key
FT	source 1..28
FEATURES	Location/Qualifiers /organism='Artificial Sequence'.
SOURCE	Location/Qualifiers 1..28 /organism="synthetic construct" /db_xref="taxon:36630"
BASE COUNT	8 a 6 c 8 g 6 t
ORIGIN	
RESULT	20
LOCUS	
DEFINITION	Query Match 100.0%; Score 24; DB 6; Length 51; Best Local Similarity 100.0%; Pred. No. 0.0016; Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
ACCESSION	
VERSION	
KWWORDS	
SOURCE	
FEATURES	
BASE COUNT	
ORIGIN	
RESULT	21
LOCUS	
DEFINITION	Query Match 95.8%; Score 23; DB 6; Length 28; Best Local Similarity 100.0%; Pred. No. 0.0069; Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
ACCESSION	
VERSION	
KWWORDS	
SOURCE	
FEATURES	
BASE COUNT	
ORIGIN	
RESULT	22
LOCUS	
DEFINITION	Query Match 95.8%; Score 23; DB 6; Length 28; Best Local Similarity 100.0%; Pred. No. 0.0069; Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
ACCESSION	
VERSION	
KWWORDS	
SOURCE	
FEATURES	
BASE COUNT	
ORIGIN	
RESULT	23
LOCUS	
DEFINITION	Query Match 95.8%; Score 23; DB 6; Length 28; Best Local Similarity 100.0%; Pred. No. 0.0069; Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
ACCESSION	
VERSION	
KWWORDS	
SOURCE	
FEATURES	
BASE COUNT	
ORIGIN	
RESULT	24
LOCUS	
DEFINITION	Query Match 95.8%; Score 23; DB 6; Length 28; Best Local Similarity 100.0%; Pred. No. 0.0069; Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
ACCESSION	
VERSION	
KWWORDS	
SOURCE	
FEATURES	
BASE COUNT	
ORIGIN	
RESULT	25
LOCUS	
DEFINITION	Query Match 95.8%; Score 23; DB 6; Length 28; Best Local Similarity 100.0%; Pred. No. 0.0069; Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
ACCESSION	
VERSION	
KWWORDS	
SOURCE	
FEATURES	
BASE COUNT	
ORIGIN	
RESULT	26
LOCUS	
DEFINITION	Query Match 95.8%; Score 23; DB 6; Length 28; Best Local Similarity 100.0%; Pred. No. 0.0069; Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
ACCESSION	
VERSION	
KWWORDS	
SOURCE	
FEATURES	
BASE COUNT	
ORIGIN	
RESULT	27
LOCUS	
DEFINITION	Query Match 95.8%; Score 23; DB 6; Length 28; Best Local Similarity 100.0%; Pred. No. 0.0069; Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
ACCESSION	
VERSION	
KWWORDS	
SOURCE	
FEATURES	
BASE COUNT	
ORIGIN	
RESULT	28
LOCUS	
DEFINITION	Query Match 95.8%; Score 23; DB 6; Length 28; Best Local Similarity 100.0%; Pred. No. 0.0069; Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
ACCESSION	
VERSION	
KWWORDS	
SOURCE	
FEATURES	
BASE COUNT	
ORIGIN	
RESULT	29
LOCUS	
DEFINITION	Query Match 95.8%; Score 23; DB 6; Length 28; Best Local Similarity 100.0%; Pred. No. 0.0069; Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
ACCESSION	
VERSION	
KWWORDS	
SOURCE	
FEATURES	
BASE COUNT	
ORIGIN	
RESULT	30
LOCUS	
DEFINITION	Query Match 95.8%; Score 23; DB 6; Length 28; Best Local Similarity 100.0%; Pred. No. 0.0069; Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
ACCESSION	
VERSION	
KWWORDS	
SOURCE	
FEATURES	
BASE COUNT	
ORIGIN	
RESULT	31
LOCUS	
DEFINITION	Query Match 95.8%; Score 23; DB 6; Length 28; Best Local Similarity 100.0%; Pred. No. 0.0069; Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
ACCESSION	
VERSION	
KWWORDS	
SOURCE	
FEATURES	
BASE COUNT	
ORIGIN	
RESULT	32
LOCUS	
DEFINITION	Query Match 95.8%; Score 23; DB 6; Length 28; Best Local Similarity 100.0%; Pred. No. 0.0069; Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
ACCESSION	
VERSION	
KWWORDS	
SOURCE	
FEATURES	
BASE COUNT	
ORIGIN	
RESULT	33
LOCUS	
DEFINITION	Query Match 95.8%; Score 23; DB 6; Length 28; Best Local Similarity 100.0%; Pred. No. 0.0069; Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
ACCESSION	
VERSION	
KWWORDS	
SOURCE	
FEATURES	
BASE COUNT	
ORIGIN	
RESULT	34
LOCUS	
DEFINITION	Query Match 95.8%; Score 23; DB 6; Length 28; Best Local Similarity 100.0%; Pred. No. 0.0069; Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
ACCESSION	
VERSION	
KWWORDS	
SOURCE	
FEATURES	
BASE COUNT	
ORIGIN	
RESULT	35
LOCUS	
DEFINITION	Query Match 95.8%; Score 23; DB 6; Length 28; Best Local Similarity 100.0%; Pred. No. 0.0069; Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
ACCESSION	
VERSION	
KWWORDS	
SOURCE	
FEATURES	
BASE COUNT	
ORIGIN	
RESULT	36
LOCUS	
DEFINITION	Query Match 95.8%; Score 23; DB 6; Length 28; Best Local Similarity 100.0%; Pred. No. 0.0069; Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
ACCESSION	
VERSION	
KWWORDS	
SOURCE	
FEATURES	
BASE COUNT	
ORIGIN	
RESULT	37
LOCUS	
DEFINITION	Query Match 95.8%; Score 23; DB 6; Length 28; Best Local Similarity 100.0%; Pred. No. 0.0069; Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
ACCESSION	
VERSION	
KWWORDS	
SOURCE	
FEATURES	
BASE COUNT	
ORIGIN	
RESULT	38
LOCUS	
DEFINITION	Query Match 95.8%; Score 23; DB 6; Length 28; Best Local Similarity 100.0%; Pred. No. 0.0069; Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
ACCESSION	
VERSION	
KWWORDS	
SOURCE	
FEATURES	
BASE COUNT	
ORIGIN	
RESULT	39
LOCUS	
DEFINITION	Query Match 95.8%; Score 23; DB 6; Length 28; Best Local Similarity 100.0%; Pred. No. 0.0069; Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
ACCESSION	
VERSION	
KWWORDS	
SOURCE	
FEATURES	
BASE COUNT	
ORIGIN	
RESULT	40
LOCUS	
DEFINITION	Query Match 95.8%; Score 23; DB 6; Length 28; Best Local Similarity 100.0%; Pred. No. 0.0069; Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
ACCESSION	
VERSION	
KWWORDS	
SOURCE	
FEATURES	
BASE COUNT	
ORIGIN	
RESULT	41
LOCUS	
DEFINITION	Query Match 95.8%; Score 23; DB 6; Length 28; Best Local Similarity 100.0%; Pred. No. 0.0069; Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
ACCESSION	
VERSION	
KWWORDS	
SOURCE	
FEATURES	
BASE COUNT	
ORIGIN	
RESULT	42
LOCUS	
DEFINITION	Query Match 95.8%; Score 23; DB 6; Length 28; Best Local Similarity 100.0%; Pred. No. 0.0069; Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
ACCESSION	
VERSION	
KWWORDS	
SOURCE	
FEATURES	
BASE COUNT	
ORIGIN	
RESULT	43
LOCUS	
DEFINITION	Query Match 95.8%; Score 23; DB 6; Length 28; Best Local Similarity 100.0%; Pred. No. 0.0069; Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
ACCESSION	
VERSION	
KWWORDS	
SOURCE	
FEATURES	
BASE COUNT	
ORIGIN	
RESULT	44
LOCUS	
DEFINITION	Query Match 95.8%; Score 23; DB 6; Length 28; Best Local Similarity 100.0%; Pred. No. 0.0069; Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
ACCESSION	
VERSION	
KWWORDS	
SOURCE	
FEATURES	
BASE COUNT	
ORIGIN	
RESULT	45
LOCUS	
DEFINITION	Query Match 95.8%; Score 23; DB 6; Length 28; Best Local Similarity 100.0%; Pred. No. 0.0069; Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
ACCESSION	
VERSION	
KWWORDS	
SOURCE	
FEATURES	
BASE COUNT	
ORIGIN	
RESULT	46
LOCUS	
DEFINITION	Query Match 95.8%; Score 23; DB 6; Length 28; Best Local Similarity 100.0%; Pred. No. 0.0069; Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
ACCESSION	
VERSION	
KWWORDS	
SOURCE	
FEATURES	
BASE COUNT	
ORIGIN	
RESULT	47
LOCUS	
DEFINITION	Query Match 95.8%; Score 23; DB 6; Length 28; Best Local Similarity 100.0%; Pred. No. 0.0069; Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
ACCESSION	
VERSION	
KWWORDS	
SOURCE	
FEATURES	
BASE COUNT	
ORIGIN	
RESULT	48
LOCUS	
DEFINITION	Query Match 95.8%; Score 23; DB 6; Length 28; Best Local Similarity 100.0%; Pred. No. 0.0069; Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
ACCESSION	
VERSION	
KWWORDS	
SOURCE	
FEATURES	
BASE COUNT	
ORIGIN	
RESULT	49
LOCUS	
DEFINITION	Query Match 95.8%; Score 23; DB 6; Length 28; Best Local Similarity 100.0%; Pred. No. 0.0069; Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
ACCESSION	
VERSION	
KWWORDS	
SOURCE	
FEATURES	
BASE COUNT	
ORIGIN	
RESULT	50
LOCUS	
DEFINITION	Query Match 95.8%; Score 23; DB 6; Length 28; Best Local Similarity 100.0%; Pred. No. 0.0069; Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
ACCESSION	
VERSION	
KWWORDS	
SOURCE	
FEATURES	
BASE COUNT	
ORIGIN	
RESULT	51
LOCUS	
DEFINITION	Query Match 95.8%; Score 23; DB 6; Length 28; Best Local Similarity 100.0%; Pred. No. 0.0069; Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
ACCESSION	
VERSION	
KWWORDS	
SOURCE	
FEATURES	
BASE COUNT	
ORIGIN	
RESULT	52
LOCUS	
DEFINITION	Query Match 95.8%; Score 23; DB 6; Length 28; Best Local Similarity 100.0%; Pred. No. 0.0069; Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
ACCESSION	
VERSION	
KWWORDS	
SOURCE	
FEATURES	
BASE COUNT	
ORIGIN	
RESULT	53
LOCUS	
DEFINITION	Query Match 95.8%; Score 23; DB 6; Length 28; Best Local Similarity 100.0%; Pred. No. 0.0069; Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
ACCESSION	
VERSION	
KWWORDS	
SOURCE	
FEATURES	
BASE COUNT	
ORIGIN	
RESULT	54
LOCUS	
DEFINITION	Query Match 95.8%; Score 23; DB 6; Length 28; Best Local Similarity 100.0%; Pred. No. 0.0069; Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
ACCESSION	
VERSION	
KWWORDS	
SOURCE	
FEATURES	
BASE COUNT	
ORIGIN	
RESULT	55
LOCUS	
DEFINITION	Query Match 95.8%; Score 23; DB 6; Length 28; Best Local Similarity 100.0%; Pred. No. 0.0069; Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
ACCESSION	
VERSION	
KWWORDS	
SOURCE	
FEATURES	
BASE COUNT	
ORIGIN	
RESULT	56
LOCUS	
DEFINITION	Query Match 95.8%; Score 23; DB 6; Length 28; Best Local Similarity 100.0%; Pred. No. 0.0069; Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
ACCESSION	
VERSION	
KWWORDS	
SOURCE	
FEATURES	
BASE COUNT	
ORIGIN	
RESULT	57
LOCUS	
DEFINITION	Query Match 95.8%; Score 23; DB 6; Length 28; Best Local Similarity 100.0%; Pred. No. 0.0069; Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
ACCESSION	
VERSION	
KWWORDS	
SOURCE	
FEATURES	
BASE COUNT	
ORIGIN	
RESULT	58
LOCUS	
DEFINITION	Query Match 95.8%; Score 23; DB 6; Length 28; Best Local Similarity 100.0%; Pred. No. 0.0069; Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
ACCESSION	
VERSION	
KWWORDS	
SOURCE	
FEATURES	
BASE COUNT	
ORIGIN	
RESULT	59
LOCUS	
DEFINITION	Query Match 95.8%; Score 23; DB 6; Length 28; Best Local Similarity 100.0%; Pred. No. 0.0069; Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
ACCESSION	
VERSION	
KWWORDS	
SOURCE	
FEATURES	
BASE COUNT	
ORIGIN	
RESULT	60
LOCUS	
DEFINITION	Query Match 95.8%; Score 23; DB 6; Length 28; Best Local Similarity 100.0%; Pred. No. 0.0069; Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
ACCESSION	
VERSION	
KWWORDS	
SOURCE	
FEATURES	
BASE COUNT	
ORIGIN	
RESULT	61
LOCUS	
DEFINITION	Query Match 95.8%; Score 23; DB 6; Length 28; Best Local Similarity 100.0%; Pred. No. 0.0069; Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
ACCESSION	
VERSION	
KWWORDS	
SOURCE	
FEATURES	
BASE COUNT	
ORIGIN	
RESULT	62
LOCUS	
DEFINITION	Query Match 95.8%; Score 23; DB 6; Length 28; Best Local Similarity 100.0%; Pred. No. 0.0069; Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
ACCESSION	
VERSION	
KWWORDS	
SOURCE	
FEATURES	
BASE COUNT	
ORIGIN	
RESULT	63
LOCUS	
DEFINITION	Query Match 95.8%; Score 23; DB 6; Length 28; Best Local Similarity 100.0%; Pred. No. 0.0069; Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
ACCESSION	
VERSION	
KWWORDS	
SOURCE	
FEATURES	
BASE COUNT	
ORIGIN	
RESULT	64
LOCUS	
DEFINITION	Query Match 95.8%; Score 23; DB 6; Length 28; Best Local Similarity 100.0%; Pred. No. 0.0069; Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
ACCESSION	
VERSION	
KWWORDS	
SOURCE	
FEATURES	
BASE COUNT	
ORIGIN	
RESULT	65
LOCUS	
DEFINITION	Query Match 95.8%; Score 23; DB 6; Length 28; Best Local Similarity 100.0%; Pred. No. 0.0069; Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
ACCESSION	
VERSION	
K	

AR131532	AR131532	21 bp	DNA	linear	PAT 16-MAY-2001	TITLE	Chimeric animal model susceptible to human hepatitis c virus infection
LOCUS	Sequence 25	from patent US 6194149.				JOURNAL	Patent: WO 0167854-A 2-20-SEP-2001;
DEFINITION						KEYWORD	Kneteman, Norman M. (CA); Tyrrell, Lorne D. (CA); Mercer, David F. (CA)
ACCESSION	AR131532					FEATURES	Location/Qualifiers
VERSION	AR131532.1	G1:14120435					1..21
SOURCE	Unknown.						
ORGANISM	Unclassified.						
REFERENCE	1. (bases 1 to 21)						
AUTHORS	Neri,B., Dong,F., Lyamichev,V., Brow,M.AnnD. and Fors,L.						
TITLE	Target-dependent reactions using structure-bridging oligonucleotides						
JOURNAL	Patent: US 6194149-A 25-27-FEB-2001;						
FEATURES	Location/Qualifiers						
BASE COUNT	6 a /organism="unknown"	7 g	3 t				
ORIGIN							
Query Match	87.5%	Score 21; DB 6; Length 21;					
Best Local Similarity	100.0%	Pred. No. 0.11; Mismatches 0; Indels 0; Gaps 0;					
Matches	21; Conservative						
Oy	1 gcagaaggctctaggatgg 21					RESULT	23
LOCUS	AR144109	21 bp	DNA	linear	PAT 08-AUG-2001	BD001049	BD001049
DEFINITION	Sequence 25 from patent US 6210880.					DEFINITION	Method and reagent for inhibiting viral replication.
ACCESSION	AR144109					ACCESSION	BD001049
VERSION	AR144109.1	GT:15105976				VERSION	BD001049.1 GT:18256068
KEYWORDS	Unknown.					KEYWORD	
SOURCE	Unknown.					SOURCE	synthetic construct.
ORGANISM	Unclassified.					ORGANISM	synthetic construct.
REFERENCE	1. (bases 1 to 21)					REFERENCE	1. (bases 1 to 21)
AUTHORS	Lyamichev,V.I., Dong,F., Brow,M.AnnD., Fors,L. and Neri,B.P.					AUTHORS	Draper,K.G., Dadykatz,L.W., Macswigen,J.A., Maysejek,D.G., Holesek,J.J. and Mamone,A.J.
TITLE	Polymerase analysis by nucleic acid structure probing with structure-bridging oligonucleotides					TITLE	Method and reagent for inhibiting viral replication
JOURNAL	Patent: US 6210880-A 25-03-APR-2001;					JOURNAL	Patent: JP 2003342285-A 209-12-DEC-2000;
FEATURES	Location/Qualifiers					COMMENT	RIBOZYME PHARMACEUTICALS INC OS Artificial Sequence
source	1..21					PN	JP 2003342285-A/209
BASE COUNT	6 a /organism="unknown"	5 c 7 g	3 t			PD	JP 2003342285-A/200
ORIGIN						PF	01-MAY-2000 JP 2000132016
Query Match	87.5%	Score 21; DB 6; Length 21;				PR	01-MAY-1992 US 07/882289, 14-MAY-1992 US 07/882712 PR
Best Local Similarity	100.0%	Pred. No. 0.11; Mismatches 0; Indels 0; Gaps 0;				14-MAY-1992 US 07/882713, 14-MAY-1992 US 07/882714 PR	
Matches	21; Conservative					14-MAY-1992 US 07/882823, 14-MAY-1992 US 07/882824 PR	
Oy	1 gcagaaggctctaggatgg 21					14-MAY-1992 US 07/882856, 14-MAY-1992 US 07/882888 PR	
Db	1 GCAGAAAGCGCTAGCCATGG 21					14-MAY-1992 US 07/882889, 14-MAY-1992 US 07/882921 PR	
RESULT	22					14-MAY-1992 US 07/882922, 14-MAY-1992 US 07/882823 PR	
AX250669	AX250669	21 bp	DNA	linear	PAT 05-OCT-2001	14-MAY-1992 US 07/882849, 14-MAY-1992 US 07/882803 PR	
LOCUS	Sequence 2 from Patent WO0167854.					14-MAY-1992 US 07/882849, 14-MAY-1992 US 07/882833 PR	
DEFINITION						14-MAY-1992 US 07/884422, 14-MAY-1992 US 07/884431 PR	
ACCESSION	AX250669					14-MAY-1992 US 07/884436, 14-MAY-1992 US 07/884521 PR	
VERSION	AX250669.1	GI:15984413				31-JUL-1992 US 07/933738, 26-DEC-1992 US 07/935854 PR	
KEYWORDS	synthetic construct.					26-AUG-1992 US 07/936086, 18-SEP-1992 US 07/943359 PR	
SOURCE	synthetic construct.					15-OCT-1992 US 07/936322, 07-DEC-1992 US 07/947129 PR	
ORGANISM	artificial sequence.					07-DEC-1992 US 07/987130, 07-DEC-1992 US 07/987133 PI	
REFERENCE	1 (bases 1 to 21)					KENNETH G DRAPER, LEC W DADYKATZ, JAMES A MACSWIGEN, PI DENNIS G MAYSEJAK, PI JAMES J HOLESKEK, ANTHONY J MAMONE, PC C12N15/09, C12N5/10, C12N7/00, C12N9/22//C12N5/10, C12R1:91, PC C12N15/00, (C12N5/00, C12R1:91)	
AUTHORS	Kneteman,N.M., Tyrell,L.D. and Mercer,D.F.					CC	
BASE COUNT	6 a /organism="taxon:32630"	5 c 7 g	3 t			FH	
ORIGIN						FT	
FEATURES	Location/Qualifiers						
source	1..21						
KEY	/organism="Artificial Sequence"						
source							

	Db	1	GCAGAAAGCCTCTAGCCATCG 21
Query Match		87.5%	Score 21; DB 6; Length 21;
Best Local Similarity		100.0%	Pred. No. 0.11; 0; Mismatches
Matches	21;	Conservative	0; Indels 0; Gaps 0;
Qy	1	gcgaaagctctacatgg 21	
Db	1	GCAGAAAGCCTCTAGCCATCG 21	
RESULT	24		
BD001478	BD001478	21 bp	RNA linear PAT 31-JAN-2002
DEFINITION	Method and reagent for inhibiting viral replication.		
ACCESSION	BD001478		
VERSTON	JP 2000342286-A/209.		
KEYWORDS			
SOURCE	synthetic construct.		
ORGANISM	synthetic construct.		
REFERENCE			
AUTHORS	Draper, K.G., Dadykisz, L.W., Macswigan, J.A., Maysejak, D.G., Holesek, J.J. and Mamone, A.J.		
TITLE	Method and reagent for inhibiting viral replication		
JOURNAL	Patent: JP 200342286-A 209 12-DEC-2000;		
COMMENT	RIBOZIME PHARMACEUTICALS INC		
OS	Artificial Sequence		
PN	JP 200342286-A/209		
PD	12-DEC-2000		
PF	01-MAY-2000 JP 200013651		
PR	11-MAY-1992 US 07/882713, 14-MAY-1992 US 07/882712 PR		
14-MAY-1992 US 07/882823, 14-MAY-1992 US 07/882824 PR			
14-MAY-1992 US 07/882886, 14-MAY-1992 US 07/882888 PR			
14-MAY-1992 US 07/882899, 14-MAY-1992 US 07/882921 PR			
14-MAY-1992 US 07/882922, 14-MAY-1992 US 07/882923 PR			
14-MAY-1992 US 07/883849, 14-MAY-1992 US 07/883850 PR			
14-MAY-1992 US 07/884074, 14-MAY-1992 US 07/884075 PR			
14-MAY-1992 US 07/884422, 14-MAY-1992 US 07/884431 PR			
14-MAY-1992 US 07/884436, 14-MAY-1992 US 07/884521 PR			
31-JUL-1992 US 07/923738, 26-AUG-1992 US 07/93854 PR			
26-AUG-1992 US 07/936086, 18-SEP-1992 US 07/943359 PR			
07-DEC-1992 US 07/963322, 07-DEC-1992 US 07/98129 PR			
KENNETH G DRAPER, LEC W DADYKIZ, JAMES A MACSWIGEN, PI DENNIS G MAYSEJAK, PI JAMES J HOLEZEK, ANTHONY J MAMONE			
PC C12N15/09, C12N5/10, C12N7/00//A61R38/43, A61R39/125, A61R39/13, A61R39/135, A61R39/145, A61K39/21, A61K39/23, A61K39/245, A61K39/29, A61K49/00, A61P1/16, A61P31/14, A61P31/16, A61P31/18, A61P31/22, A61P35/02, C12O1/58, PC (C12N15/09, C12R1:93), C12N5/00, C12N5/00, A61K37/48, (C12N15/00, PC C12R1:93)			
CC			
FH			
FT			
FEATURES			
source	Location/Qualifiers		
FT	1. .21 /organism="synthetic construct" /db_xref="taxon:32630"		
BASE COUNT	6 a 5 c 7 g 3 t		
ORIGIN			
Qy	1 gcgaaagctctacatgg 21		
Query Match		87.5%	Score 21; DB 6; Length 21;
Best Local Similarity		100.0%	Pred. No. 0.11; 0; Mismatches
Matches	21;	Conservative	0; Indels 0; Gaps 0;
Qy	1 gcgaaagctctacatgg 21		
RESULT	25		
BD05672	AX250672	Sequence 5 from Patent WO0167854.	DNA linear PAT 05-OCT-2001
DEFINITION	ACCESSION AX250672		
ACCESSION	VERSION AX250672.1		
KEYWORDS			
SOURCE	synthetic construct.		
ORGANISM	synthetic construct.		
REFERENCE			
AUTHORS	1 (bases 1 to 24)		
TITLE	Kneteman, N.M., Tyrrell, L.D. and Mercer, D.F.		
JOURNAL	Chimeric animal model susceptible to human hepatitis c virus infection		
COMMENT	Patent: WO 0167854-A 5 20-SEP-2001; Kneteman, Norman M. (CA); Tyrrell, Lorne D. (CA); Mercer, David F. (CA)		
FEATURES			
source	Location/Qualifiers		
BASE COUNT	6 a 5 c 8 g 5 t		
ORIGIN			
Query Match		87.5%	Score 21; DB 6; Length 24;
Best Local Similarity		100.0%	Pred. No. 0.1; 0; Mismatches
Matches	21;	Conservative	0; Indels 0; Gaps 0;
Qy	4 gaaagctctacatgg 24		
Db	1 GAAGGGTCAGCCATGGG 21		
Search completed: August 26, 2002, 21:20:52			
Job time: 7706 sec			

Tue Aug 27 15:49:41 2002

us-10-037-990a-1.oli.rge

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OM nucleic - nucleic search, using sw model

Run on: August 26, 2002, 19:44:36 ; Search time 3233.25 Seconds
(without alignments)
100.186 Million cell updates/sec

Title: US-10-037-990a-1
Perfect score: 24
Sequence: 1 gcagaaaggcttagccatggcgt 24

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 13736207 seqs, 6748477542 residues

Word size : 21

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0
Maximum DB seq length: 100

Post-processing: Listing first 65 summaries

Database : EST:*
1: em_estba:/*
2: em_esthum:/*
3: em_estin:/*
4: em_estmu:/*
5: em_estov:/*
6: em_estpl:/*
7: em_estro:/*
8: em_hrc:/*
9: gb_est1:/*
10: gb_est2:/*
11: gb_htc:/*
12: gb_gss:/*
13: em_gss_hum:/*
14: em_gss_inv:/*
15: em_gss_pn:/*
16: em_gss_vrt:/*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Score	Match Length	DB ID	Description
------------	-------------	--------------	-------	-------------

No matches found

Search completed: August 26, 2002, 22:14:58
Job time: 9022 sec

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GenCore version 4.5

OM nucleic - nucleic search, using sw model
Run on: August 26, 2002, 22:14:58 ; Search time 3233.25 Seconds
(without alignments)
87.663 Million cell updates/sec

Title: US-10-037-990a-3
Perfect score: 21
Sequence: 1 gtcgtgcagcccccaggaccc 21
Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0
Searched: 13736207 seqs, 6748477542 residues
Word size : 21

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0

Maximum DB seq length: 100

Post-processing: Listing first 65 summaries

Database :	EST.*
1:	em_estba:*
2:	em_esthum:*
3:	em_estin:*
4:	em_estmu:*
5:	em_estov:*
6:	em_estpl:*
7:	em_estro:*
8:	em_htc:*
9:	gb_est1:*
10:	gb_est2:*
11:	gb_htc:*
12:	gb_gss:*
13:	em_gss_hum:*
14:	em_gss_inv:*
15:	em_gss_pln:*
16:	em_gss_vrt:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Score	Match Length	DB ID	Description

No matches found

Search completed: August 26, 2002, 22:14:58
Job time: 9022 sec

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OM nucleic - nucleic search, using sw model

Run on: August 26, 2002, 22:17:12 ; Search time 119.4 Seconds

(without alignments)
 43.202 Million cell updates/sec

Title: US-10-037-990a-3

Perfect score: 21

Sequence: 1 gtcgtgcggccggacc 21

Scoring table: OLIGO_NTC

Gapop 60.0 , Gapext 60.0

Searched: 383533 seqs, 122816752 residues

Word size : 21

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0

Maximum DB seq length: 100

Post-processing: Listing first 65 summaries

Database : Issued_Patents_NA.*

1: /cggn2_6/prodata/2/ina/5A_COMB_seq:*

2: /cggn2_6/prodata/2/ina/5B_COMB_seq:*

3: /cggn2_6/prodata/2/ina/6A_COMB_seq:*

4: /cggn2_6/prodata/2/ina/6B_COMB_seq:*

5: /cggn2_6/prodata/2/ina/pcmvs_COMB_seq:*

6: /cggn2_6/prodata/2/ina/backfile1.seq:*

Pred No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
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No matches found

Search completed: August 26, 2002, 22:17:12
 Job time: 5905 sec

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FEATURES		KESSLER CHRISTOPH (DE); BARTL KNUT (DE)
source		Location/Qualifiers 1. .27 /organism="synthetic construct" /db_xref="taxon:32630"
BASE COUNT	5 a 8 c 9 g 9 9	5 t
ORIGIN		
RESULT	3	
LOCUS	AX003946	
DEFINITION	Sequence 6 from Patent WO9923249.	48 bp
ACCESSION	AX003946	DNA
VERSION	AX003946.1	linear
KEYWORDS		PAT 24-AUG-2000
SOURCE		
ORGANISM		Hepatitis C virus.
VIRUS		Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae; Hepacivirus.
REFERENCE		1. (bases 1 to 48)
AUTHORS		Kessler,C., Bartl,K., Haberhausen,G. and Orum,H.
TITLE		Specific and sensitive nucleic acid detection method
JOURNAL		Patent; WO 9923249-A 14-MAY-1999;
FEATURES		KESSLER CHRISTOPH (DE); BARTL KNUT (DE); HABERHAUSEN Gerd (DE); ROCHE DIAGNOSTICS GMBH (DE); ORUM HENRIK (DK)
source		Location/Qualifiers 1. .48 /organism="Hepatitis C virus" /db_xref="taxon:11103"
BASE COUNT	9 a 18 c 14 g 7 t	
ORIGIN		
RESULT	4	
LOCUS	AX003947	
DEFINITION	Sequence 7 from Patent WO9923249.	48 bp
ACCESSION	AX003947	DNA
VERSION	AX003947.1	linear
KEYWORDS		PAT 24-AUG-2000
SOURCE		
ORGANISM		Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
REFERENCE		1. (bases 1 to 48)
AUTHORS		Kessler,C., Bartl,K., Haberhausen,G. and Orum,H.
TITLE		Specific and sensitive nucleic acid detection method
JOURNAL		Patent; WO 9924606-A 20-MAY-1999;
FEATURES		KESSLER CHRISTOPH (DE); BARTL KNUT (DE); HABERHAUSEN Gerd (DE); ROCHE DIAGNOSTICS GMBH (DE); ORUM HENRIK (DK)
source		Location/Qualifiers 1. .48 /organism="Homo sapiens" /db_xref="taxon:606"
BASE COUNT	9 a 17 c 14 g 8 t	
ORIGIN		
RESULT	5	
LOCUS	AX021565	
DEFINITION	Sequence 3 from Patent WO9924606.	48 bp
ACCESSION	AX021565	DNA
VERSION	AX021565.1	linear
KEYWORDS		PAT 07-SEP-2000
SOURCE		
ORGANISM		Hepatitis C virus.
VIRUS		Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae; Hepacivirus.
REFERENCE		1. (bases 1 to 48)
AUTHORS		Kessler,C., Bartl,K., Haberhausen,G. and Orum,H.
TITLE		Specific and sensitive nucleic acid detection method
JOURNAL		Patent; WO 9924606-A 3 20-MAY-1999;
FEATURES		KESSLER CHRISTOPH (DE); BARTL KNUT (DE); HABERHAUSEN Gerd (DE); ROCHE DIAGNOSTICS GMBH (DE); ORUM HENRIK (DK)
source		Location/Qualifiers 1. .48 /organism="Hepatitis C virus" /db_xref="taxon:11103"
BASE COUNT	9 a 18 c 14 g 7 t	
ORIGIN		
RESULT	6	
LOCUS	AX021566	
DEFINITION	Sequence 4 from Patent WO9924606.	48 bp
ACCESSION	AX021566	DNA
VERSION	AX021566.1	linear
KEYWORDS		PAT 07-SEP-2000
SOURCE		
ORGANISM		human.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
REFERENCE		1. (bases 1 to 48)
AUTHORS		Kessler,C., Bartl,K., Haberhausen,G. and Orum,H.
TITLE		Specific and sensitive nucleic acid detection method
JOURNAL		Patent; WO 9924606-A 4 20-MAY-1999;
FEATURES		KESSLER CHRISTOPH (DE); BARTL KNUT (DE); HABERHAUSEN Gerd (DE); ROCHE DIAGNOSTICS GMBH (DE); ORUM HENRIK (DK)
source		Location/Qualifiers 1. .48 /organism="Homo sapiens" /db_xref="taxon:606"
BASE COUNT	9 a 17 c 14 g 8 t	
ORIGIN		

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OM nucleic - nucleic search, using sw model

Run on : August 26, 2002, 21:20:54 ; Search time 1915.63 Seconds

(without alignments)
229,406 Million cell updates/sec

Title: US-10-037-990a-3

Perfect score: 21

Sequence: 1 gtcgtgcagccctccaggaccc 21

Scoring table: Oligo_NUC

Gapext 60.0 , Gapext 60.0

Searched: 1797656 seqs, 10463268293 residues

Word size : 21

Total number of hits satisfying chosen parameters: 10

Minimum DB seq length: 0

Maximum DB seq length: 100

Post-processing: listing first 65 summaries

Database : GenEmbl:*

1: gb.ba: *
2: gb_htg: *
3: gb_in: *
4: gb_on: *
5: gb_ov: *
6: gb_pat: *
7: gb_ph: *
8: gb_pl: *
9: gb_pr: *
10: gb_ro: *
11: gb_sts: *
12: gb_sy: *
13: gb_un: *
14: gb_vl: *
15: em_ba: *
16: em_fun: *
17: em_hum: *
18: em_in: *
19: em_mu: *
20: em_on: *
21: em_or: *
22: em_lv: *
23: em_pat: *
24: em_ph: *
25: em_pl: *
26: em_ro: *
27: em_sts: *
28: em_un: *
29: em_vl: *
30: em_htg_hum: *
31: em_htg_inv: *
32: em_htg_other: *
33: em_htg_inv: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

ALIGNMENTS

RESULT	1	C	1	21	100-0	21	6	AX147016	AX147016 Sequence
		C	2	21	100-0	27	6	BD00273	BD00273 Oligonucleotide
			3	21	100-0	48	6	AX03946	AX03946 Sequence
			4	21	100-0	48	6	AX03947	AX03947 Sequence
			5	21	100-0	48	6	AX021565	AX021565 Sequence
			6	21	100-0	48	6	AX021575	AX021575 Sequence
			7	21	100-0	48	6	AX021576	AX021576 Sequence
			8	21	100-0	48	6	AX021631	AX021631 Sequence
			9	21	100-0	48	6	AX021632	AX021632 Sequence

RESULT	1	REFERENCE	1	Roche Diagnostics GmbH (DE)	LINEAR	PAT	08-JUN-2001
		AUTHORS		,Weindel,K., Rieding,M. and Geiger,A.			
		TITLE		Magnetic glass particles, method for their preparation and uses thereof			
		JOURNAL		Location/Qualifiers			
		FEATURES		1. 21			
		SOURCE		/organism="synthetic construct"			
				/db_xref="taxon:37630"			
				/note="Synthetic oligonucleotide probe (HCV)"			
				/note="Ruthenium3+-(tris-bipyridyl)-derivatisation"			
				/mod_base=OTHER			
				/mod_base=OTHER			
QY	1	BASE COUNT	3	a	9	c	6
		ORIGIN			9	g	3
		RESULT	2				
		LOCUS	BD00273/c	DEFINITION	100-0%; Score 21; DB 6; Length 21;		
				Best Local Similarity	100-0%; Pred. No. 0-042;		
				Matches	Mismatches 0;		
					Indels 0;		
					Gaps 0;		
Db	1	1	ggttgtgcagccctccaggaccc 21				

Query Match 100-0%; Score 21; DB 6; Length 21;
Best Local Similarity 100-0%; Pred. No. 0-042;
Matches 21; Conservative 0; Mismatches 0;
Indels 0; Gaps 0;

27 bp DNA linear PAT 31-JAN-2002
Oligonucleotide primers for efficient detection of hepatitis C virus (HCV) and methods of use thereof.
ACCESSION BD00273
VERSION JP 2000279200-A/11.
KEYWORDS BD00273.1 GI:18623352

SOURCE 1 GTCGTGCAGCCCTCCAGGACCC 21
ORGANISM synthetic construct.
REFERENCE 1 (bases 1 to 27)
AUTHORS Lynen,J.M. and Gorman,K.M.
TITLE Oligonucleotide primers for efficient detection of hepatitis C virus (HCV) and methods of use thereof
PATENT JP 2000279200-A 11 10-OCT-2000;
JOURNAL ORTHO CLINICAL DIAGNOSTICS INC
COMMENT OS Artificial Sequence
PN JP 2000279200-A/11
PD 10-OCT-2000
PP 03-FEB-2000 JP 2000032656

SUMMARIES

Result No.	Score	Query Match Length	DB ID
8	10463268293	1797656	